95WO-US08894.

14-JUL-1995;

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01-FEB-1996

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/*tag= a
/note= "forms doubled stranded segment when
bound to nucleotides 5-22 of the
sequence given in AAT12342"
                                                        Disclosure; Page 447; 720pp; French.
                                                                                                                                                                                                           1616 TAAAATATATTTGTT 1631
         (MOLE-) MOLECULAR ENGINES LAB.
                                                                                                                                                                                                                                             AAT32141 standard; DNA; 18 BP
17-SEP-2001; 2001FR-0011978.
                                                                                                                                                                                                                    17 TAAATATAATTIGAT 2
                                                                                                                                                                                                                                                                16-SEP-1996 (first entry)
                            WPI; 2003-313353/30.
                                                                                                                                                                                                                                                                                                                    nisc_feature
                                                                                                                                                                                                                                                                                                                                                 WO9602673-A1
                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                      AAT32141;
                                                                                                                                                                                                                                   RESULT 136
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The present sequence is an example of a complementary sense strand (primer/linker), which comprises a priming site, labelling region, cohesive and and comprises a priming site, labelling region, cohesive end and complementary strand. The priming site is the cohesive end and complementary strand. The priming site is the cohesive end and complementary strand. The priming site is the copy labelling region is a template sequence which directs DNA polymerase to incorporate multiple labelled, e.g. radioactive complementary strand provides compatible ends for ligation of prinkers to restriction fragments. The complementary strand provides a region of double stranded DNA which is required by DNA ligases for the attachment of the prinker to a restriction fragments.

A prefd, sequencing procedure comprises the generation of restriction fragments from the DNA mol. to be sequenced, ligation of prinkers to the fragments, conc. and buiffer exchange, stranded restriction fragments, conc. and buiffer exchange, generation and sepn. of sequencing prods., exposure of X-ray film to sequencing prods. and detection of the signal on the film.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haematopoietic cell proliferation disorder related oligonucleotide #660.
                                                                                                                                                                                                                                                                                                                                                                               New oligo:nucleotide(s) for DNA sequencing - having a priming site, a labelling region and a cohesive end complementary to a restriction fragment sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; probe; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.2%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 2.2e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 BP; 14 A; 2 C; 1 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 5; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABZ10520 standard; DNA; 18 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       616 ACAAAAAACAACAAAT 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ACABABACBABART 17
                                                                                                                                                                                             (AMIC-) AMICON INC.
(GRAC ) GRACE & CO-CONN W R.
                                                                                                               94US-0275169.
94US-0202400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                        WPI; 1996-105934/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
Synthetic.
                                                                                                         14-JUL-1994;
25-FEB-1994;
                                                                                                                                                                                                                                                                                  seonard JT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABZ10520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 137
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel isolated 17 mer mucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel condend or detecting, identifying, quantifying and/or amplifying a mucleic acid, for detecting, identifying, quantifying and/or amplifying a mucleic acid, as one component of a gene chip, in vitro as (anti) sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schiz Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for disagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequence represents a tumour suppression therapy. This polymucleotide sequence represents a tumour suppression related human fukutin oligomucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                      New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sense strand, DNA sequencing; oligonucleotide; prinker;
primer; linker; priming site; labelling region; cohesive end;
complementary strand; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.2%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 2.1e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 7 A; 1 C; 1 G; 8 T; 0 other;
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Gaps

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26-MAR-2002; 2002WO-EP03401

#O200277272-A2.

03-OCT-2002.

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Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides -
                         Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T;
Pelet C, Schwope I, Ziebarth H;
                                                                                                                    Claim 15; Page 48; 117pp; English
26-MAR-2001; 2001US-278333P
               (EPIG-) EPIGENOMICS AG.
                                                                 WPI; 2003-018942/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9507983-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
20-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ89232;
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 138
                                                                                                                                                                                                                                                                                                                                                                                                     AAQ892.
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The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regularcy regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated cpG for distinguishes between methylated and non-methylated CpG represent specifically claimed mucleoic acid. ABZ09861 to ABZ1118 represent specifically claimed mucleoide sequences from the present invention. Oligonucleoides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute invention can be used for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can be used for detecting a predisposition to, differentiation between acute of the present invention can be used for detecting a predisposition to, differentiation of the present invention of the present invention of the present invention and the present invention and the present invention and the present invention the present invention and proportion of the present invention and proportion of the present invention of the present invention and proportion of the present invention and proportion of the present invention of the present invention and proportion of the present invention and proportion of the present invention of the present invention of the present invention and proportion of the present invention of the present invention and proportion of the present invention of the present invention of the present invention and proportion of the present invention and proportion o ö enables subclasses, diagnosis, prognosis, treatment and/or monitoring of harmatopoietic cell proliferative disorders. The present method enable a highly specific classification of harmatopoietic cell proliferative disorders allowing for improved and informed treatment of patients. Gaps ó Sequence 18 BP; 4 A; 0 C; 4 G; 10 T; 0 other;

Query Match 1.2%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 2.2e+02; Matches 15; Conservative 0; Mismatches 1; Indels

Rat opioid receptor PCR primer. AAQ89232 standard; cDNA; 20 BP (updated)
(first entry)

Opioid receptor; gene therapy; diagnostic; primer; PCR; polymerase chain reaction; ss. polymerase chain

94WO-US10358

PCR using the degenerate primers given in AAQ89231-32 was used demonstrate that the relative mRNA abundance of mu, delta and kappa opioid receptors, and of a new opioid family member (AAQ89233) in rat brain, was 68, 14, 10 and 8%, respectively. (Updated on 25-MAR-2003 to correct PN field.) New nucleic acid encoding new human mu opioid receptor - and related vectors, transformed cells, antibodies etc., useful in diagnosis, treatment and drug screening. Sequence 20 BP; 5 A; 2 C; 4 G; 7 T; 2 other; Example 9; Page 154; 266pp; English 93US-0120601. (INDV) UNIV INDIANA FOUND WPI; 1995-131351/17 13-SEP-1993; Query Match Yo L;

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Gaps Streptococcus pyogenes großL antisense oligonucleotide SEQ ID NO:332. ö 1.2%; Score 14.4; DB 1; Length 20; 75.0%; Pred. No. 2.4e+02; tive 2; Mismatches 3; Indels 1121 GTTATAAAGATGTTATAGTA 1140 1 GCTRTRAACATGTTGTAGTA 20 AAH56684 standard; DNA; 20 BP. (first entry) Local Similarity 75.0 es 15; Conservative 06-SEP-2001 AAH56684; RESULT 139 AAH56684

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Antisense oligonucleotide; groE1, groE5; inhibitor; growth; microorganism; Escherichia col1; Streptococcus pneumoniae; diagnosis; Streptococcus pyogenes, Staphylococcus aureus; Pseudomonas aeruginosa; antibacterial; antiviral; antiproliferative; antisense therapy; microbial infection; ss. (GENE-) GENESENSE TECHNOLOGIES INC. ä 20-NOV-2000; 2000WO-CA01347. 18-NOV-1999; 99US-0166249 Streptococcus pyogenes. Wright JA, Young AH, WPI; 2001-355633/37. W0200136625-A2 25-MAY-2001

Novel antisense compounds targeting nucleic acid encoding groEL or groES gene of microorganism, which hybridize with and inhibit expression of the genes, useful to inhibit growth of microorganism Claim 3; Page 50; 110pp; English. having the

The present invention specifically claims AAH56168 to AAH56832 which are antisense oligonucleotides to nucleotide sequences encoding groB. More

The invention relates to SAPL [SIT4-(sporulation-induced transcript4) associated proteins-likel polypeptide, selected from SAPLa polypeptide isoforms and SAPLa polypeptide isoforms. The SAPL polynucleotides are useful in gene therapy for treating and preventing insulin-dependent diabetes mellitus (IDDM). Fragments of the SAPL DNA are useful as primers and probes. The SAPL polypeptides are useful in screening for a substance e.g., a peptide or chemical compound, which interacts and/or binds with them. Sequences AAF83318-350 represent PCR primers specific for the SAPL

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Claim 14; Page 98; 129pp; English.

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of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a microorganism, where the antisense compound is complementary to GL or a microorganism and specifically hybridises with and inhibits the expression of GL or GS, is claimed. (I) have antibacterial, antiviral and antiprolliferative activities, and can be used in antisense therapy and for inhibition of expression of GL or GS in cells or tissues in vitro. (I) are also useful for inhibiting expression of GL or GS in cells or tissues in vitro. (I) are also useful for inhibiting the growth of a microorganism, or inhibiting the expression of GL or GS and concernation or inhibiting the expression of GL or GS and microorganism (a bacterial cell or a virus) having a GL or GS gene which involves administering to the microorganism or to a cell infected with the microorganism of CC a virus) having a mammalian pathological condition mediated by microorganism having a GL or GS gene which involves identifying a evexyotic organism or to a cell infected with the microorganism having a GL or GS gene which involves identifying a evexyotic organism or to a cell infected by microorganism having a GL or GS gene and administering (I) such that the growth of microorganism is inhibited. The antiense compounds are utilised for diagnostics, the microorganism having a GL or GS gene and administering (I) such that the growth of microorganism is inhibited. The antiense compounds are utilised for diagnostics, the prevent or delay microbial infections in humans. They are also useful as molecular weight markers. Addisologics on Addisologics or Addisologics or organism the present invention. They are used in the exemplification of the present invention.
antisense compounds (I) comprising antisense oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 15 A; 4 C; 1 G; 0 U; 0 other;
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   8488888888888888888888888888
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Gaps

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1; Indels

0; Mismatches

1097 AGAAGATGAATCATTG 1112

15; Conservative

Matches

4 AGAAGATGAATCCTTG 19

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Length 20;

1.2%; Score 14.4; DB 1; Local Similarity 93.8%; Pred. No. 2.4e+02;

Query Match

Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 other;

1.2%; Score 14.4; DB 1; Length 20; 93.8%; Pred. No. 2.46+02; Live 0; Mismatches 1; Indels . . 633 4 AAAAAACAACAAACAA 19 618 AAAAAACAACAAATAA Conservative Local Similarity see 15; Conserv Matchee ઠે g

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Gaps

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AAF83325 standard; DNA; 20 AAF83325; RESULT 140 AAF83325

Human SAPL cDNA specific primer 4dest4 6f. 09-JUL-2001 (first entry)

SAPL; SIT4; SIT4 associated proteins like; human; antidiabetic; sporulation-induced transcript 4; SAPLa; SAPLb; gene therapy; IDDM; insulin-dependent diabetes mellitus; PCR primer; ss.

Homo sapiens.

WO200129213-A1.

26-APR-2001.

19-OCT-2000; 2000WO-GB04027.

99US-0160400.

19-0CT-1999;

(WELL) WELLCOME TRUST LTD. (MERI) MERCK & CO INC.

Hammond H; Caskey CT, Hey P, Hey P, Twells RCJ, Hess JW, WPI; 2001-300338/31. Metzker ML; Fodd JA,

Isoforms of novel gene arising from alternative splicing and encoding highly related proteins termed as SAPLa and SAPLb, from the IDDM4 locus on human chromosome 11q13, useful for treating IDDM and other diseases

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The present sequence is a PCR primer used in a method for shuffling genes cry2Aa, cry2Ab and cry2Ac. Gene shuffling is a process for generating recombinant nucleic acids. Oligonucleotide assisted approaches can be used to produce family shuffled nucleic acids without isolating or cloning full-length homologous nucleic acids. Family gene shuffling oligonucleotides are provided by aligning homologous nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombining homologous nucleic acids to produce family shuffle nucleic acids comprises hybridizing and elongating a set of family gene shuffling oligonuclectides and providing a population of recombined nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                         Minshull J, Bass SH, Welch M, Ness JE;
                                                                                                                                  Cry2Aa; Cry2Ab; Cry2Ac; family gene shuffling; recombinant; nucleic acid diversity; mutagen synthesis; PCR primer; ss.
                                                                                                       Cry2A family gene shuffling PCR primer 1 for.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Page 54; 74pp; English.
                        AAA62676 standard; DNA; 19 BP.
                                                                                                                                                                                                                                                                                    99US-0116447,
99US-0118813.
99US-0118854.
99US-0141049.
99US-0408392.
99US-0408393.
                                                                                                                                                                                                                                                           18-JAN-2000; 2000WO-US01203.
                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Crameri A, Stemmer WPC,
Gustafsson C, Patten PA;
                                                                                                                                                                                                                                                                                                                                                                                                               (MAXY-) MAXYGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-482862/42.
                                                                                                                                                                                                     WO200042561-A2
                                                                             08-JAN-2001
                                                                                                                                                                           Inidentified
                                                                                                                                                                                                                                                                                                    05-FEB-1999;
05-FEB-1999;
24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                       12-OCT-1999;
12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                           28-SEP-1999;
                                                                                                                                                                                                                                  20-JUL-2000
                                                                                                                                                                                                                                                                                       19-JAN-1999
                                                    AAA62676;
RESULT 141
           AAA626
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1 GICTITGALTITATGGAAA 19

BP.

AAH58297 standard; DNA; 19

RESULT 143

AAH58297

AAH58297;

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acid sequences to select conserved regions of sequence identity and regions of sequence diversity. A plurality of oligonucleotides are synthesized which correspond to at least one region of sequence diversity. In this example, the oligonucleotides were spiked into the assembling mix and PCR was then performed using the present primer. The method can be used to produce a family of shuffled mucleic acids, to produce recombinant molecules with greater molecular diversity and to generate classical mutagens. Homologous nucleic acids with low sequence similarity and non-homologous nucleic acids are also easily recombined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, FCNA and Cyclin B1.
Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme is useful for The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNR and Cyclin B1
                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
                                                                                                                                                                                                      Score 14.2; DB 1;
Pred. No. 2.5e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 5 A; 1 C; 4 G; 9 T; 0 other;
                                                                                                                                                                        Seguence 19 BP; 9 A; 0 C; 3 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barber JR, Robbins JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 57; 109pp; English.
                                                                                                                                                                                                                                                                           1102 ATGAATCATTGATTGAATA 1120
                                                                                                                                                                                                                                                                                                           1 Arcaaraarcrarrcaara 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cdk7 ribozyme binding site #56
                                                                                                                                                                                                          1.18;
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                                                                                                                                                                                                                                                                                                                                                                                               AAA83135 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-DEC-2000 (first entry)
                                                                                                                                                                                                                      Local Similarity 84.2
nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tritz R, Welch PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMU-) IMMUSOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-412314/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA83135;
                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                            RESULT 142
AAA83135
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The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme [1] which cleaves RNA encoding a cytchkine involved in inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule [11] comprising a promoter operally linked to a nucleic acid segment encoding [1]. [1] can have antipsoriatic, chuleic acid segment encoding [1]. [1] can have antipsoriatic, dermatological, cytostatic, antiseborrhaic, antidiabetic, antisickling, dermatological, vulnerary, keratolytic and virucide activities, and cleaves RNA encoding cytokine involved in inflammation. [1] can be used in gene therapy. [1] and [1] are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, appearance or seased for treating proliferative eye diseases such as diabetic retinopathy, virucoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing scarring such as keloid, adhesion and hypertrophic or hypertrophic burn scar. AAM57577 to AAM62099 represent sequences used in the exemplification of the present invention.
                                                                                                                                                    Ruman; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnerary; proliferative disease; skin disease, psoriasis; diabetic retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP; matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide; antisickling; ophthalmological; keratolytic; gene therapy; viral wart; atopic dermatitis; actinic keratosis; squamous cell carcinoma; basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar; sickle cell retinopathy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating proliferative shin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent
                                                                                                                 Cell-cycle dependent kinase cdk7 ribozyme binding site SEQ ID NO:721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.1%; Score 14.2; DB 1; Length 19;
4.2%; Pred. No. 2.5e+02;
ve 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 124; 408pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.1%;
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-2000; 2000WO-US29500.
                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robbins JM, Tritz R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-300427/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IMMU-) IMMUSOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200130362-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                   sapiena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-1999;
                                                                                 10-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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Gaps

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Gaps

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/ Match 1.1%; Score 14.2; DB 1; Length 19; Local Similarity 84.2%; Pred. No. 2.5e+02; les 16; Conservative 0; Mismatches 3; Indels

Query Match

1574 GTTTCTGATTGTATGGAAA 1592

à

BP.

ABZ10313 standard; DNA; 19

RESULT 145 ABZ10313

schultz143-3.rng

(first entry)

16-JAN-2003

ABZ10313;

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(+)-delta-cadinene 8-hydroxylase (designated as CYP706B1), and the present inventor that the control of gossypol and related sesquiterpenes in cotton seeds through genetic engineering techniques. The polymucleotide sequence encoding CYP706B1 is useful in suppression of the biosynthesis of gossypol and related sesquiterpenes in cotton seeds, where the polymucleotide sequence is expressed in antisense or sense orientation as a perfect match to the native gene whose expression is sought to be suppressed. The polymucleotide sequence of the invention is useful for producing cotton cultivates which avoid the presence of sesquiterpenoids in their seeds, and for producing cotton seed product which is suitable for use as a feed for both livestack and humans.

The present sequence represents a PCR primer used to clone cDNA encoding cotton CYP706B1 in the examples of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel cotton (+)-gamma-cadinene 8-hydroxylase polypeptide designated as CYP706B1, useful as target for suppression of biosynthesis of gossypol formation in cotton seeds -
                                                                                                                                                                                                                                                                                                 biosynthesis of gossypol; sesquiterpene; cotton seed; cotton cultivate; sesquiterpenoid; livestock feed; PCR; primer; ss.
                                                                                                                                                                                                                                                                               Cotton; (+)-delta-cadinene 8-hydroxylase; CYP706B1; cytochrome P450;
                                                                                                                                                                                                                                         PCR primer LP132R used to clone cDNA encoding cotton CYP706B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to the isolation of cotton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19 BP; 3 A; 1 C; 8 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang Y;
1574 GITTCTGATTGTATGGAAA 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 4; 26pp; English.
                             Greirigaritriaregaaa 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Luc P,
                                                                                                                           ABX93225 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2002; 2002US-0067534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-FEB-2001; 2001US-267160P.
                                                                                                                                                                                                       30-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESSENBERG M
CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-341036/32.
                                                                                                                                                                                                                                                                                                                                                         Gossypium arboreum.
                                                                                                                                                                                                                                                                                                                                                                                             US2002187538-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LUOP/) LUO P.
(WANG/) WANG Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Basenberg MK,
                                                                                                                                                                                                                                                                                                                                                                                                                               12-DEC-2002
                                                                                                                                                                 ABX93225;
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(CHEN/)
                                                                                         RESULT 144
                                                                                                         ABX93225,
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The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gane and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 represent specifically claimed nucleotide sequences from the present invention. Oligomucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute upelogenous leukaemia; as probes for determining the cytcsine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the related sequences and their complements; and as primers for the related sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subconderic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative a highly specific classification of haematopoietic cell proliferative cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders.
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                                                                                                                  Haematopoietic cell proliferation disorder related primer SEQ ID NO:453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides -
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                                                                                                                                                           Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; probe; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J; Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E; Lewin A, Lipscher E, Maier S, Model P, Mueller V, Otto T; Pelet C, Schwope I, Ziebarth H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%; Score 14.2; DB 1;
84.2%; Pred. No. 2.5e+02;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19 BP; 7 A; 9 C; 0 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 35; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           476 TGTGGGTCTGTTGTAGGGT 494
                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-2002, 2002WO-EP03401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2001; 2001US-27833P.
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Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-018942/01.
                                                                                                                                                                                                                                                                                                                       #0200277272-A2.
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                03-OCT-2002.
                                                                                                                                                                                                                                                                              Synthetic.
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1.1%; Score 14.2; DB 1; Length 19; llarity 84.2%; Pred. No. 2.5e+02; Conservative 0; Mismatches 3; Indels

Local Similarity tes 16; Conserv

Best Loca Matches

Query Match

563 ACCATGAAATATCCAGAAC 581

ACCATCAATCTCCAGCAC 1

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RESULT 14 AAQ75568/

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Screening for polymorphism by amplification of pooled nucleic acid - restriction with endonuclease(s), sepn. of fragments and comparison of restriction patterns, for detecting disease related mutation(s), in genetic mapping etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalian lysosomal trafficking regulators LYST1, Lyst1, LYST2 and
Lyst2 - useful to diagnose Chediak-Higashi syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lystl; mouse; lysosomal trafficking regulator; beige; bg gene;
Chediak-Higashi syndrome; CH syndrome; sequence tagged site; STS;
D13S£k8; yeast artificial chromosome; YAC; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                             A TaqI polymorphism at the CCAATT box of the human tyrosinase gene was identified by amplification of the 5' promoter region using the primers given in AAQ91528-29, and examination of the restriction patterns of the amplified products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This oligonucleotide comprises a reverse primer sequence for
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 14.2; DB 1; Length 20;
Pred. No. 2.7e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse bg critical region YAC STS D13Sfk8 reverse primer.
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 4 A; 8 C; 1 G; 7 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 68; 237pp; English
                                                                                                                                                                                                                                                                                Example 3; Page 28; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              964 TIGIGAGGACATGIGGAAG 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trereaccactacaccase 2
                                                                                 (CLAR-) CLARKE INST PSYCHIATRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT74234 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                          1.1%;
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96US-0033599.
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                                                 93US-0157269.
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           94CA-2136705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 84.2
Matches 15; Conservative
                                                                                                                     Petronis A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barbosa-Alleyne MDFS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYPL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-402616/37.
                                                                                                                                                     WPI; 1995-255407/34.
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20-DEC-1996;
               25-NOV-1994;
                                                 26-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-1997;
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                                                                                                                     Kennedy JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A method for the analysis of cDNA comprises (a) preparing an aggregate of mRNAs and represente of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GRNSES) (iles AAQ75547-07598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Restriction fragment length polymorphism, RFLP; point mutation, mapping; primer; polymerase chain reaction; PCR; tyrosinase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                              Analysis; gene expression; reverse transcription; primer; cDNA;
                                                                                                                                                                            Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.1%; Score 14.2; DB 1; Length 20;
44.2%; Pred. No. 2.7e+02;
ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 5; 11pp; Japanese.
                                                                                                                                                                                                                                 aggregate; restriction enzyme; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  615 TACAAAAACAACAATAA 633
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                                                                      AAQ75568 standard; DNA; 20 BP.
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                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Conservative
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                          04-AUG-1995
                                                                                                                                                                                                                                                                                                     JP06303997-A.
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                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
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RESULT 14 AAQ91529/

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
novel sequence tagged site (STS) D13Sfk8. It produces a 143 bp amplicon when used with a D13Sfk8 forward primer (see AAT74212). Novel STS were isolated from murine beige (Bg) critical region yeast artificial chromosomes by interspersed repetitive element (IRE)-PCR (D13Sfk1-D13Sfk12) or by direct selection (D13Sfk13-D13Sfk19). Characterisation of the bg critical region in murine chromosome 13 and positional cloning of bg were performed as an antecedent to identification of the homologous human gene LYST1 (see AAT74201), which is mutated in human Chediak-Higashi syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Production of capped RNA or analogues - useful as substrates for influenza virus associated virally encoded endonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ö
                                                                                                                                                                                                                                                                                                                                                                                Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                1.1%; Score 14.2; DB 1;
84.2%; Pred. No. 2.7e+02;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= c
/mod_base= 2'-O-methyluridine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag= a
mod_base= 7-methylguanosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= b
/mod_base= triphosphorylated
                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 7 A; 6 C; 2 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olsen DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5' fragment #2 of alfalfa mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page 12; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       792 TAAATTTTGCCATAAAGTC 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TAATGCTGCCATAACTC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-AUG-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 84.2
hes 16, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-051868/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9640159-AL
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Matches
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capped RNA or analogue is an influenza endonuclease aptamer, useful for treating or preventing an influenza infection in an animal. The synthetic capped RNA are substrates for virally encoded endonuclease associated with influenza virus. The short non-extendible (due to their length or because of the modification of the 3' end of the oligo) RNA molecules are potent inhibitors of the cleavage of capped RNA by influenza endonuclease. They may be used to investigate viral and cellular mechanisms of transcription/translation, or mRNA maturation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primers AAZ01426-Z06209 were used to amplify open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01455). These ORFs anchode polypeptides (see AAY36754-Y37949) which can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye trachomatis is responsible for a large number of diseases uch as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholnihits; pneumopathy in breast feeding infants; and veneraal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer; bartholinitis; pneumopathy; venereal lymphogramulomatosis; ss.
                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                 Similarity 21.1%; Score 14.2; DB 1; Length 20; Similarity 21.1%; Pred. No. 2.7e+02; 4; Conservative 12; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer used to amplify an ORF of Chlamydia trachomatis.
                                                                                                                                                                                Sequence 20 BP; 3 A; 1 C; 2 G; 14 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 20 BP; 7 A; 5 C; 5 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                 1519 GCTTTATATTTTAACTTT 1537
                                                                                                                                                                                                                                                                                                                    GCUUUUAUUUAAUUU 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 1824; 1755pp;
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97FR-0015041.
97FR-0016034.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ06093 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-371125/31.
                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ06093;
                                                                                                                                                                                                                       Query Match
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Respiratory disease; pneumonia; bronchitis; heart disease; sarco sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.

Synthetic. Chlamydia pneumoniae.

WO9927105-A2

PCR primer used to amplify an ORF of Chlamydia pneumoniae.

(first entry)

13-SEP-1999

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AAX96384 standard; DNA; 20

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                                                                                                                                                                                                                                                                                                                  Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primers AAZ01426-Z06209 were used to amplify open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs accode polygeptides (see AAY36754-Y37949) which can be used as vaccines against Chlamydia trachomatis. Attisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, and inclusion conjunctivitis; genital diseases such as mongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, hartholimitis; pneumopathy in breast feeding infants; and venereal lymphogramulomatosis. The polypeptides of the invention may be of use in treating these diseases.
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 Length 20;
                                                                                                                                                                                                                                                                                  PCR primer used to amplify an ORF of Chlamydia trachomatis.
                                 3: Indels
Ouery Match 1.1%; Score 14.2; DB 1; Best Local Similarity 84.2%; Pred. No. 2.7e+02; Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 3 A; 2 C; 6 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 1448; 1755pp; English.
                                                                   1319 CCTAGTTTGATACTCCCAG 1337
                                                                                     20 CCTTGTTTGATATGCCCAG 2
                                                                                                                                                                                     AAZ01504 standard; DNA; 20 BP
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97FR-0015041.
97FR-0016034.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                       AAZ01504;
                                                                                                                                                       RESULT 151
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Genome sequence of Chlamydia pneumoniae Page 1822; Disclosure; 1912pp; English.

WPI; 1999-357842/30.

(GEST) GENSET 04-NOV-1998; 21-NOV-1997;

Griffais R;

98WO-IB01890 98US-0107078. 97FR-0014673.

20-NOV-1998;

03-JUN-1999

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                                                                                                                                                                                                                                                                                                                                                                                                           AAX91991-X97517 represent PCR primers used to amplify open reading frames and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent contributing factor in heart disease, sarcoidosis, sinusitis, purulent by the open reading frames of the C. pneumoniae genome (see AAX94584-AAX95879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 2.7e+02; iive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermostable polypeptide factor; DNA synthesis activity; DNA polymerase; in vitro DNA synthesis; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      968 GAGGACATGTGGAAGCACT 986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX15294 standard; DNA; 20
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Matches 16; Conservative
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Gaps

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1518 GGCITTATATTTTAACTT 1536

Best Local Similarity 84.2%; Matches 16; Conservative

Query Match

GGCGTTATGTGTTTAACTT 19

RESULT 152 AAX96384/c

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Mukai H,

07-JAN-1999

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The present PCR primer was used in the course of the invention. The specification describes Pyrococcus furiosus thermostable polypeptide factors. These factors bind to, and promote the DNA synthesis activity of DNA polymerase. The polymerase related factors can be used to provide more efficient in vitro DNA synthesis and amplification systems (e.g. for polymerase chain reaction) by using the factors in conjunction with a DNA polymerase.
                                                                                                                                                                                         Thermostable polypeptide factors promoting the activity of DNA polymerase - for improvement of DNA synthesis and amplification in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermostable polypeptide factors promoting the activity of DNA polymerase - for improvement of DNA synthesis and amplification in
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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DNA polymerase; in vitro DNA synthesis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 5 A; 2 C; 4 G; 9 T; 0 other;
                                                                                                                            Miyake K,
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                                                                                                                            Fujita T, Kato I,
                                   98WO-JP02845.
                                                            97JP-0320692.
                                                                                                  (TAKI ) TAKARA SHUZO CO LID
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                                     24-JUN-1998;
                                                              21-NOV-1997;
                                                                         26-JUN-1997;
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26-JUN-1997;
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Uemori T;
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Uemori T;
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Amplification of a foreign gene by recombining close to a recombination hot spot and autonomously replicating sequence and culturing in the presence of a replication fork inhibitor protein for efficient foreign gene expression
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                                                     The present PCR primer was used in the course of the invention. The specification describes Pyrococcus furiosus thermostable polypeptide factors. These factors bind to, and promote the DNA synthesis activity of DNA polymerase. The polymerase related factors can be used to provide more efficient in vitro DNA synthesis and amplification systems (e.g. for polymerase chain reaction) by using the factors in conjunction with a DNA polymerase.
                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                      Length 20;
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                                                                                                                                                                                                                                    Query Match
1.1%; Score 14.2; DB 1; Length 2
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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Pred. No. 2.7e+02;
                                                                                                                                                                                                    Sequence 20 BP; 9 A; 4 C; 2 G; 5 T; 0 other;
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                               Example 9; Page 128; 177pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA38895 standard; DNA; 20
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                    Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1; disease diagnosis; 88.
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    Mismatches
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                                            441 CTTCAAGCAAATCTACTTC 459
                                                                                CSTCCATCAATCTACTTC 19
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    16; Conservative
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AAH80901/c
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AC AAH809
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Matches
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    Natches
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AAC AAHB

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The present invention describes a method for predicting the potential of an oligonucleotide to hybridise to a (complementary) target nucleotide sequence, involving identifying a subset of oligonucleotides within the predetermined number of unique oligonucleotides based on the evaluation of the parameter. Oligonucleotides in the subset are identified that are clustered along a region of the nucleotide sequence that is hybridisable to the target nucleotide sequence. This is useful for evaluating oligonucleotide probe sequences. The present sequence is an oligonucleotide described in the exemplification of the invention.
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Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1; disease diagnosis; ss.
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Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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                                                                                             Human immunodeficiency virus type 1.
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Kincaid

Webb PG,

Delenstarr GC,

Wolber PK,

schultz143-3.rng

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The present invention describes a method for predicting the potential of an oligonucleotide to hybridise to a (complementary) target nucleotide sequence, involving identifying a subset of oligonucleotides within the predetermined number of unique oligonucleotides based on the evaluation of the parameter. Oligonucleotides in the subset are identified that are clusterred along a region of the nucleotide sequence that is hybridisable to the target nucleotide sequence. This is useful for evaluating oligonucleotide probe sequences. The present sequence is an oligonucleotide described in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 10 A; 3 C; 3 G; 4 T; 0 other;
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                                                                    WPI; 2001-424456/45
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Shannon KW,
                                                                                                                                                                                                                                                      parameters
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Kincaid

Webb PG,

Delenstarr GC,

98US-0021701 98US-0021701

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The present invention specifically claims AAH56368 to AAH56832 which are antisense oligonucleotides to nucleotide sequences encoding groß. More generally, antisense compounds (I) comprising antisense oligonucleotides of 5-50 bases targeted to a nucleotide sequence encoding groß. (heat shock protein (HSP)60) (GL) and groß (HSP10) (GS) gene from a nicroorganism, where the antisense compound is complementary to GL or GS of a microorganism and specifically hybridises. with and inhibite the expression of GL or GS, is claimed. (I) have antibacterial, antiviral and antiproliferative activities, and can be used in antisense therapy and for inhibition of expression of groß or groß. (I) are useful for inhibition the growth of a microorganism, or inhibiting the growth of a microorganism, or inhibiting cross useful for inhibiting the growth of a microorganism, (I). (I) are a virus) having a GL or GS gene which involves administering to the microorganism or to a cell infected with the microorganism cross a cell infected with the microorganism or to a cell infected with the microorganism or to a cell infected with the microorganism swinch involves identifying a cukaryotic organism having a pathological condition mediated by microorganism and the advisory or antiple organism which involves deminisms having a GL or GS gene with the microorganism or to a cell infected with the microorganism which involves identifying a cukaryotic organism having a pathological condition mediated by microorganism and the advisory or antiple or the average or a pathological condition mediated by microorganism and the advisory or antiple or and the microorganism and the advisory or antiple or and the microorganism and the advisory or antiple or and the microorganism and the advisory or antiple or and the microorganism and the advisory or antiple or and the microorganism and the advisory or antiple or and the microorganism and the advisory or antiple or and the advisory or antiple or and a cell inference or and the advisory or antiple or and a cell
  is hybridisable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense oligonucleotide; groE, groEs; inhibitor; growth; microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis; Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa; antibacterial; antiviral; antiproliferative; antisense therapy;
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel antisense compounds targeting nucleic acid encoding großL or großS gene of microorganism, which hybridize with and inhibit expression of the genes, useful to inhibit growth of microorganism having the genes -
clustered along a region of the nucleotide sequence that is hybric to the target nucleotide sequence. This is useful for evaluating oligonucleotide probe sequences. The present sequence is an oligonucleotide described in the exemplification of the invention.
                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S. aureus groß operon antisense oligonucleotide SEQ ID NO:356
                                                                                                                                                                                         Length 20;
                                                                                                                                                                                       Score 14.2; DB 1; Length 2
Pred. No. 2.7e+02;
0; Mismatches 3; Indels
                                                                                                                                       Sequence 20 BP; 11 A; 3 C; 2 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENESENSE TECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 51; 110pp; English.
                                                                                                                                                                                                                                                                                                   977 TGGAAGCACTTTAAGTTTT 995
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                                                                                                                                                                                                                                                                                                                                               TGGTTGCACTTTAAATTTT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                al Similarity 84.2%;
16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH56708 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                microbial infection; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wright JA, Young AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-355633/37.
                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression of the having the genes
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                                                                                                                                                                                               Query Watch
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1.1%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 2.7e+02; ative 0; Mismatches 3; Indels

ABS67672 standard; DNA; 20 BP.

ss; antisense therapy; casein kinase-2 alpha; cytostatic; antidiabetic; antiinflammatory; diabetes; hyperproliferative disorder; cancer; human; breast cancer; prostate cancer; liver cancer; infection; inflammation;

cumour; mouse

Homo sapiens

Casein kinase-2 antisense oligonucleotide ISIS127172

(first entry)

29-NOV-2002

/label= CTHER /note= "All cytidines are 5-methylcytidine. Phosphorothioate backbone"

Location/Qualifiers

Key modified_base

1..20 /*tag= 8 /label= 0

/note= "2'-methoxyethyl nucleotides' 16..20 /*tag= c /label= OTHER /note= "2'-methoxyethyl nucleotides"

modified_base

1..5 /*tag= b /label= OTHER

modified base

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McKay R, Freier SM, Wyatt

WPI; 2002-627521/67.

08-FEB-2001; 2001US-0780172 31-JAN-2002; 2002WO-US02942

WO200262818-A2

PHARM INC

SISI (-SISI)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to performing a thermal cycle of PCR by using a substrate on which a deoxyribonucleic acid (DNA) is immobilized. The method is useful in the medical, biochemical, molecular biological and generic engineering fields. Sequences ABQ79871-881 represent PCR primers used in the method of the invention.
or GS gene and administering (I) such that the growth of microorganism is inhibited. The antisense compounds are utilised for diagnostics, therapeutics, prophylaxis and as research reagents and kits, e.g., to prevent or delay microbial infections in humans. They are also useful as molecular weight markers. AAH56362 to AAH56567 and AAH56833 to AAH56854 exemplification of the present invention. AAH56855 to AAH56897 exemplification of the present invention. AAH56855 to AAH568970 represent groß nucleotide sequence given in the present invention.
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carrying out a thermal cycle of polymerase chain reaction (PCR) by using a substrate on which a DNA is immobilized used in medical, biochemical, molecular biological and gene engineering fields
                                                                                                                                                                                                                         ö
                                                                                                                                                                                          Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymerase chain reaction, thermal cycle, immobilisation, genetic engineering; PCR; primer; ss.
                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                       Ouery Match
1.1%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3;
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                                                                                                                                                      Sequence 20 BP; 3 A; 5 C; 2 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of a PCR primer #1
                                                                                                                                                                                                                                                          1566 TTITTACTGTTTCTGATTG 1584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Examples; Page 9; 13pp; Japanese.
                                                                                                                                                                                                                                                                              BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-DEC-2000; 2000JP-0399573.
                                                                                                                                                                                                                                                                                                                                                                              ABQ79871 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KOHAN CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TOJO ) TOYO KOHAN CK
(TAKA/) TAKAHASHI K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-630904/68.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                ABQ79871;
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The invention relates to a compound 8-50 nucleobases in length targeted to a nucleic acid molecule encoding casein kinase 2-alpha. The compound specifically hybridises with and inhibits the expression of casein kinase 2-alpha, or specifically hybridises with at least an thinase 2-alpha, or specifically hybridises with at least an 8-aucleobase portion of an active site on a nucleic acid molecule encoding casein kinase 2-alpha i.e. an antisense oligonucleotide.

Also included are: (1) a composition comprising the compound and a carrier or diluent; (2) inhibiting the expression of casein kinase carpha in cells or tissues by contacting the cells or tissues with the novel compound; and (3) treating an animal having a disease or condition associated with casein kinase 2-alpha by administering to the animal the compound cited above so that expression of casein kinase 2-alpha is compound cited above so that expression of casein kinase 2-alpha is conficted any and compounds are useful for modulating the expression of casein kinase 2-alpha and for treating diseases or conditions associated with expression of casein kinase 2-alpha, e.g. diabetes or hyperproliferative disorder, particularly cancer, such as breast cancer, prostate cancer, or liver cancer. The antisense breast cancer, prostate cancer, or liver cancer. The antisense compounds are also useful for diagnostics, therapeutise, prophylaxis, compounds are also useful for diagnostics, therapeutise, prophylaxis, compounds are also useful for diagnostics, therapeutise, prophylaxis, casearch reagents and kits, and in distinguishing between functions of various members of a biological pathway. The present equence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense oligonucleotides targeted to nucleic acid encoding casein kinase 2-alpha, useful in diagnostic and research applications, or for treating a disease or condition associated with expression of casein kinase 2-alpha
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Gaps

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1.1%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 2.7e+02; ative 0; Mismatches 3; Indels

Query Match
Best Local Similarity 84.2
Matches 16; Conservative

618 AAAAAACAACAAATTT 636

AAAAAAAAAAAAAATTT 1

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RESULT 162 ABS67672/c

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; 9s; antisense; cellular apoptosis susceptibility gene; antiinflammatory; antitumour; cytostatic; CAS; CSEI; CSP; charactory; antitumour; cytostatic; CAS; CSEI; CSP; chromosome 20q13; mitosis; apoptosis; proliferation; cancer; importin-alpha; nuclear localisation; cell cycle; pyperproliferative disorder; degenerative disorder; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; ALS; retinitis pigmentosa; blood cell disorder; gene therapy; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "CTHER = phosphorothicate backbone, all cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense compound that hybridizes and inhibits nucleic acid encoding cellular apoptosis susceptibility gene, useful for treating a hyperproliferative disorder such as cancer
                                                                                                                         Gaps
casein kinase-2 alpha antisense oligomucleotide of the invention.
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/mcd_bage= "OTHER"
/mcd_e= "OTHER = 2'-0-methoxyethyl nucleotides"
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/*tag=
/= Add base= "OTHER"
/note= "OTHER = 2'-O-methoxyethyl nucleotides"
                                                                                   Length 20;
                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human CAS gene antisnese oligonucleotide, ISIS 128210.
                                                                            / Match 1.1%; Score 14.2; DB 1; Local Similarity 84.2%; Pred. No. 2.7e+02; les 16; Conservative 0; Mismatches 3;
                                    Sequence 20 BP; 5 A; 3 C; 5 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            claim 3; Page 91; 135pp; English.
                                                                                                                                                                    438 AAACTICAAGCAAATCTAC 456
                                                                                                                                                                                                    19 AGACTICAAGCAATTGTAC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-2000; 2000US-0705299.
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                                                                                                                                                                                                                                                                                                                    ABS59257 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cowsert LM, Freier SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-608254/65.
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modified_base
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                                                                                                                                                                                                                                                                                                                                                               ABS59257;
                                                                                   Query Match
                                                                                                                         Matches
                                                                                                                                                                                                                                                                              RESULT 163
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cc 20013. CAS has been implicated in the regulation of mitosis, apoptosis and cellular proliferation and is highly expressed in some cancer cells. CAS has also been shown to mediate export of importin-alpha is a nuclear import receptor for nuclear nucleus. Importin-alpha is a nuclear import receptor for nuclear cansort is involved in cell cycle defects. The antisense compounds specifically hybridise with, and inhibit expression of the gene or specifically hybridise with an 8 nucleobase portion of its active site. The antisense compounds are useful for inhibiting the expression of a cellular apoptosis susceptibility gene in cells or tissues and for treating an animal having a disease or condition associated with a cellular apoptosis susceptibility gene, where the disease or condition is a hyperproliferative disorders such as ancer, preferably breast or colon cancer, degenerative disorders such as ancer, preferably breast or colon cancer, degenerative disorders such as Alzheimer's disease, Parkinson's concer, degenerative disorders such as ancer, preferably breast or colon cancer, degenerative disorders such as sancer, preferably breast or colon cancer, degenerative disorders such as alzheimer's disease, anytirophic lateral sclerosis (Ais), retinitis pigmentosa and blood cell disorders. The compounds are also useful for diagnostics, therapeutica, prophylaxis, as research reagents and kits, for the prophylaxis, as research reagents and kits, for antisense gene therapy and prophylactically (e.g. to prevent or delay inference therapy and prophylactically (e.g. to prevent or delay inference in ABSS9252-ABSS9322 are targeted to the human CAS gene.
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antisense oligonuclectide; diabetes; obesity; skeletal muscle disorder;
inflammation; tumour formation; phosphorothioate backbone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention comprises antisense oligonucleotides designed to inhibit expression of Syntaxin 4 interacting protein. The antisense oligonucleotides of the invention are useful for inhibiting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel antisense compound that hybridizes and inhibits nucleic acid molecule encoding Syntaxin 4 interacting protein, useful for treating diabetes, obesity and skeletal muscle disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 1.1%; Score 14.2; DB 1; Length 20; Local Similarity 84.2%; Pred. No. 2.7e+02; neg 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 8 A; 3 C; 3 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1307 TGAACTAACAATCCTAGTT 1325
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84

expression of Syntaxin 4 interacting protein in cells or tissues. The antisense oligonucleotides are also useful for treating an animal having a disease or condition associated with Syntaxin 4 interacting protein (e.g. diabetes, obesity or a skeletal muscle disorder). The antisense oligonucleotides can also be used to prevent or delay infection, inflammation and tumour formation. The present DNA sequence represents a human Syntaxin 4 interacting protein antisense oligonucleotide.

NOTE: The present sequence contains a phosphorothicate backbone and 2'-0-methoxyethyl wings. Human translocating chain-associated membrane protein, RT-PCR primer #2. New human transposition chain related membrane protein and its coding Human; translocating chain-associated membrane protein; BioTRAM; i.1%; Score 14.2; DB i; Length 20 84.2%; Pred. No. 2.7e+02; vative 0; Mismatches 3; Indels Sequence 20 BP; 10 A; 1 C; 2 G; 7 T; 0 other; reverse transcriptase PCR; RT-PCR primer; 88. (SHAN-) SHANGHAI SHENGYUAN GENE DEV CO LID. Example 3; Page 12; 22pp; Chinese. 1045 TATTTATGEATTTAA 1063 19 TATTICTGTATACATTTAA 1 멾. 24-FBB-2000; 2000CN-0111729. 24-FEB-2000; 2000CN-0111729 AAS18578 standard; DNA; 20 12-MAR-2002 (first entry) Local Similarity 84.2 nes 16; Conservative WPI; 2002-034947/05. Mao Y, Xie Y; Homo sapiens 29-AUG-2001. CN1310184-A. AAS18578; seguence Query Match Matches 88888888888 ठ

tumour, The invention relates to a novel human translocating chain associating membrane protein (BioTRAM), polynucleotides encoding this polypeptide praces used to produce the polypeptide. The present invention also discloses the method of applying the polypeptide and polynucleotides in treating immunological disorder, malignant tumour cancer and other diseases. The antagonist resisting the polypeptide and its treatment effect is also disolosed. Diagnosis and determination method based on the discrimination of the mutation in the nucleic acid sequence and the change in the polypeptide expression level, and the application of the polypeptide septession level, and the sequence represents a reverse transcriptase (RT)-PCR primer used to isolate the coding sequence of the novel human BioTRAM protein as described in the invention.

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Length 20,
                                          1.1%; Score 14.2; DB 1;
84.2%; Pred. No. 2.7e+02;
Sequence 20 BP; 8 A; 0 C; 1 G; 11 T; 0 other;
                                            Query Match
Best Local Similarity
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ö Phospholipase A2 group IIA; synovial; antisense modulation; inflammation; phospholipase A2 group IIA inhibitor; phosphorothicate; antiinflammatory; antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer; psoriasis; diabetes; ss. Gaps Mouse phospholipase A2 antisense oligonucleotide SEQ ID NO:108. ö Indels ٠. ش 0; Mismatches Location/Qualifiers 609 20 ACC47011 standard; DNA; 20 BP 591 TGTAAAGTATTATTTT 05-JUN-2003 (first entry) 16; Conservative *tag= Key modified_base Mus musculus. Synthetic. ACC47011; 4 RESULT 166 Matches ACC47011 ð 셤

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Gaps

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Length 20;

25-MAY-2001; 2001US-0865866. 21-MAY-2002; 2002WO-US16135. (ISIS-) ISIS PHARM INC. 05-DEC-2002

WO200297133-A1

note= "2'-0-methoxyethyl (2'-MOB) gapmer" 16..20 /*tag= c /note= "2'-0-methoxyethyl (2'-MOB) gapmer"

/mod_base= OTHER

*tag= b

modified base

modified_base

'note= "phosphorothioate backbone"

'mod_base= OTHER

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Bennett CF, Wyatt JR;

WPI; 2003-140495/13.

New compound that hybridizes with and inhibits the expression of Phospholipase A2, group IIA, useful for preparing a composition for treating or preventing inflammation, cancer, psoriasis or diabetes

Claim 3; Page 89; 135pp; English.

The present invention describes a compound (I) comprising 8-50 nucleobases which is targeted to a 5' untranslated region (UTR). Coding, 19 untranslated region (UTR). Coding, 19 untranslated region of a nucleic acid molecule encoding phospholipase 3' group IIA (synovial), where the compound specifically hybridises with and inhibits the expression of phospholipase A2, group IIA (synovial).

Also described: (I) a composition comprising the compound and a carrier or diluent; (2) a method of inhibiting the expression of phospholipase A2, group IIA in cells or tissues, and (3) a method of treating an animal having a disease or condition associated with phospholipase A2, and antipsoriatic activities, and can be used in vaccines and in gene threapy. The compound (I) can be used for preparing a composition for treating or preventing inflammation, cancer, psoriasis or diabetes. The present sequence represents a mouse phospholipase A2 group IIA (synovial)

diabetes, multiple sclerosis,

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autoimmune arthritis, autoimmune insulinitis or crohn's disease), cancer, or a disease/disorder caused by aberrant apoptosis. They are also useful for diagnostics, therapeutics, prophylaxis or as research reagents or kits. The invention is useful in gene therapy. The present sequence is an antisense oligonucleotide targetted to human IFNGR2 DNA.
                                                                               Seguence 20 BP; 6 A; 2 C; 5 G; 7 T; 0 other;
disorder (e.g. autoimmune thyroiditis,
                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-2002.
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ID AATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to antisense compounds, composition and methods for modulating the expression of human interferon gamma receptor 2 (IFWGR2). The compositions comprise antisense compounds targetted to nucleic acids encoding IFWGR2. Antisense compounds invention are useful for treating diseases or conditions associated with IFWGR2, e.g. autoimmune
chimeric phosphorothioate antisense oligonucleotide, which is used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense oligonucleotides for modulating Interferon gamma receptor 2, particularly useful for treating autoimmune disorders (e.g. multiple sclerosis or Crohn's disease), cancers or diseases caused by aberrant
                                                                                   Gapa
                                                                                                                                                                                                                                                                                     Antisense, interferon gamma receptor 2; autoimmune disorder, cancer autoimmune thyroiditis; autoimmune insulinitis; multiple sclerosis; diabetes; autoimmune arthritis; Crohn's disease; apoptosis; IFNGR2; gene therapy; prophylaxis; human; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Phosphorothioate backbone; All cytidine residues are S-methylcytidines"
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                                                           Length 20;
                                                                                  3; Indels
                                                                                                                                                                                                                                                               Human IFNGR2 antisense oligonucleotide, ISIS #142809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mod_base= OTHER
/note= "2'-methoxyethyl mucleotides"
16..20
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/note= "2'-methoxyethyl nucleotides"
                                                         1.1%; Score 14.2; DB 1;
ilarity 84.2%; Pred. No. 2.7e+02;
Conservative 0; Mismatches 3;
                                   Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 15; Page 86; 127pp; English
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             example from the present invention.
                                                                                                         690 ATTGGGCCAAGGCCCAAGA 708
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                                                                                                                               1 ATTGAGCCAAAGGCCATGA 19
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                                                                                                                                                                                AAD52331/c
ID AAD52331 standard; DNA;
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                                                                      Local Similarity
Les 16; Conserv
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modified_base
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                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insect resistant cotton plants, tissues and seeds that include the MONIS985 event, useful in plant insect protection and plant breeding
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1.1%; Score 14.2; DB 1; Length 20; 84.2%; Pred, No. 2.7e+02; tive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3' end of the cotton genomic remnant DNA
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                                                                                                                     437 GAAACTICAAGCAAAICTA 455
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                                                                  16; Conservative
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                                    Best Local Similarity
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(updated)
(first entry)

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Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA; Modak A, Pavco P, Beigleman L, Sullivan SW, Sweedler D; Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves TWF-alpha mRNA at the nucleotide base position indicated in the DB line. Regions of the mRNA that do not form secondary folding
                                                                                              Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha: respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogencus leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atheroselerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
                                                                         Mouse TNF-a hammerhead ribozyme target sequence (nt position 1310)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ribozymes having modified bases and methods for producing them for use in inhibiting disease related genes
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                                                                                                                                                                                                                                                             Mus musculus.
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16-AUG-1994;
17-AUG-1994;
19-AUG-1994;
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04-NOV-1994;
10-NOV-1994;
28-NOV-1994;
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23-DEC-1994;
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                                    25-MAR-2003
                                                14-MAY-1997
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15-APR-1994
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29-MAR-1994
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                                                                                                                                                                                                                                   AIDS; ss.
           AAT56320;
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95WO-IB00156

9405-0201109 9408-0201109 9408-0224483 9408-0224483 9408-0225861 9408-0257858 9408-0271280 9408-0291832 9408-0291832 9408-0291832 9408-0301839 9408-0301839 9408-03080000 9408-031486 9408-031486 9408-031486 9408-031486 9408-031486 9408-031489

94US-0357577 94US-0363233

94US-0334847 94US-033760B 94US-0345516

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                                                                                                                                                                                                                                                                                                                                                                                                                                       Human TNR-alpha hammerhead ribozyme target sequence (nt position 1269).
                                                                                                                                                                                                         Gaps
         ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit TNF-alpha expression, making them potentially useful for treating rheumatoid arthritis, septic shock and other inflammatory disorders including psoriasis, as well as for treatment of AIDS.

(Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bnzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TMF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; theumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
                                                                                                                                                                                                           ö
structures and that contain potential hammerhead and hairpin
                                                                                                                                                                           1.1%; Score 14; DB 1; Length 15; 28.6%; Pred. No. 2.2e+02; tive 10; Mismatches 0; Indels
                                                                                                                                                     Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
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940'S - 0218934
940'S - 0228934
940'S - 0224483
940'S - 0228041
940'S - 0245736
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940'S - 0291433
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(first entry)
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Best Local Similarity 28.0%
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25-MAR-1997
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15-APR-1994;
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19-AUG-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human TNF-alpha bammerhead ribozyme target sequence (nt position 1258).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                               Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Meswiggen JA; Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D; Thompson JD, Tracz D, Usman N, Wincott FB, Woolf T;
                                                                                                                                                                                                                                                                      The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and Hairpin structures and that contain potential hammerhead and Hairpin ribozymes cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit TNF-alpha expression, making them potentially useful for treating rheumatoid arthritis, septic shock and other inflammatory disorders including psoriasis, as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; LL-5; ICMM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TWF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; TAFAnallocation; chronic myellogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction, stroke; restenosis; myocardial infarction; stroke; restenosis; myocardial infarction; stroke; sextenosis; myocardial ischaemia; Ramsabai disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                         Ribozymes having modified bases and methods for producing them for use in inhibiting disease related genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 28.6%; Pred. No. 2.2e+02;
Matches 4; Conservative 10; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
                                                                                                                                                                                                                                                Claim 2; Page 243; 407pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT55796 standard; RNA; 15 BP
94US-0321993.
94US-0334847.
94US-0337608.
94US-0345516.
94US-0357577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1038 TATTATTAT 1051
                                                                                          (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : |:::|::|::|:
1 UAUUUAUUAUUAU 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {updated}
(first entry)
                                                                                                                                                                                  WPI; 1995-351090/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
25-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9523225-A2
               04-NOV-1994;
10-NOV-1994;
                                         28-NOV-1994;
                                                    16-DEC-1994;
23-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT55796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIDS;
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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves FNF-alpha mRNA at the nucleotide base position indicated in the DE line.

Or sequence of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis.

Or Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit TNF-alpha expression, making them potentially useful for treating rheumatoid arthritis, septic shock and other inflammatory disorders including psoriasis, as well as the target of treatment of ALDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA; Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D; Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribozymes having modified bases and methods for producing them for use in inhibiting disease related genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Match 1.1%; Score 14; DB 1; Length 15; Local Similarity 28.6%; Pred. No. 2.2e+02; les 4; Conservative 10; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15 BP; 4 A, 0 C; 0 G; 11 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 242; 407pp; English.
                                                                 9405-0201109-9405-0218934-9405-022795-9405-022795-9405-0227958-9405-0228041-9405-0271280
                                                                                                                                                                                                                                                                                                                                     940S-0293520
940S-0393520
940S-0310303
940S-0311486
940S-0311749
940S-0316771
940S-0316731
940S-0316731
940S-0316731
                                                                                                                                                                                                                                                                  94US-0291932.
94US-0291433.
94US-0292620.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0337608
94US-0345516
  95WO-IB00156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0363233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0357577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : |:::|::|:
1 UAUUUAUUAUUAU 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-OCT-1994;
07-OCT-1994;
11-OCT-1994;
04-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-DEC-1994;
23-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-NOV-1994;
28-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                            08-SEP-1994;
                                                                                                                                                                                              5-APR-1994
                                                                                                                                                                                                                        18-MAY-1994
                                                                                                                                                                                                                                                                                                 16-AUG-1994;
                                                                                                                                                                                                                                                                                                                                             19-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                23-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                       02-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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cancer; genetic drift; detection; mutation; 88.

Homo sapiens WO9833893-A2 06-AUG-1998. 98WO-US00730. 97US-0985162. 97US-0036476.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel isolated nucleic acid molecule comprising a variant gene associated with an eating disorder and selected from any of 119 polymorphisms with their corresponding genotyping in dataset, alleles and HGBASE identification, given in the specification. The novel nucleic acid molecule has polymorphisms in the serotonin receptor ID, delta-opioid receptor, or dopamine receptor D2, which is useful in diagnostic and prognostic assays for eating disorders, in particular anorexia nervosa and bullmia nervosa. This polymucleotide sequence represents a hypocretin receptor I PCR primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecule having polymorphisms in the serotonin receptor 1D, delta-opioid receptor, or dopamine receptor D2, useful in diagnostic and prognostic assays for eating disorders, such as anorexia
                                                                                                      polymorphism; dataset; allele; HGBASE identification;
                                                                                                                 serotonin receptor 1D; delta-opioid receptor; dopamine receptor D2; anorexia nervosa; bulimia nervosa; PCR; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.1%; Score 14; DB 1; Length 16; 00:0%; Pred. No. 2.3e+02;
                                                                               Hypocretin receptor 1 PCR primer SEQ ID No 91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16 BP; 3 A; 6 C; 3 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 61; 149pp; English.
            ABT34305 standard; DNA; 16 BP
                                                                                                                                                                                                                                                            20-JUL-2001; 2001US-306440P.
13-NOV-2001; 2001US-331285P.
19-DBC-2001; 2001US-340843P.
19-DEC-2001; 2001US-340844P.
                                                                                                                                                                                                                                                 2001US-305153P
                                                                                                                                                                                                                         16-JUL-2002; 2002WO-US22555
                                                          (first entry)
                                                                                                                                                                                                                                                                                                                      (PRIC-) PRICE FOUND LTD
                                                                                                                                                                                                                                                                                                                                             Yeager M;
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-268122/26.
                                                                                                                                                                                                                                                                                                                                                                                                                               and bulimia nervosa
                                                                                                       disorder;
                                                                                                                                                                           WO2003012143-A1
                                                                                                                                                                                                                                                16-JUL-2001;
                                                                                                                                                      Unidentified
                                                          12-JUN-2003
                                                                                                                                                                                                  13-FEB-2003.
                                                                                                                                                                                                                                                                                                                                              Bergen AW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                   ABT34305;
                                                                                                      Bating
 ABT34305
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Enzymatic nucleic acids - which cleave RNA derived from an epidermal growth factor receptor, useful for inhibiting cell proliferation and

McSwiggen JA;

Fell P,

Akhtar S,

WPI; 1998-437449/37

(RIBO-) RIBOZYMB PHARM INC. (UYAS-) UNIV ASTON.

04-DEC-1997; 4-JAN-1998;

Claim 5; Page 82; 109pp; English.

for treating cancers

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The present invention describes enzymatic nucleic acid molecules (NAMS) which specifically cleave RNA derived from an epidermal growth factor receptor (EGR-R) gene. ARV9721 to AAV99633 and AAV9989 to AAV99090 represent specifically claimed target sequence from human BGP-R. AAV9804 to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and halpin ribozymes respectively for human BGP-R. The NAMS are useful for cleaving SGP-R RNA in the treatment of a condition associated with EGPR expression levels e.g. to inhibit cell proliferation in the prevention or treatment of cancers. The NAMS can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of BGP-R RNA in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buman, aryl hydrocarbon nuclear transport, ARNT, TIE-2, angiogenesis; integrin alpha 6 subunit, integrin subunit beta 3; hairpin ribozywe; harmerhead ribozywe; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiathritic; antipsociatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; periasis; verrue andiotibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Integrin subunit beta 3 substrate sequence SEQ ID NO:6033.
                                                                                                                                                                                                                                                                                                                                                                   Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                   1.1%; Score 14; DB 1; 1
78.6%; Pred. No. 2.5e+02;
ive 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                        Sequence 17 BP; 9 A; 1 C; 2 G; 5 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA22807 standard; RNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1599 AGTAAATATGAAAC 1612
                                                                                                                                                                                                                                                                                                                                                                                              78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:|||:||:|||
AGUAAAUAUGAAAC 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 78.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9950403-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA22807;
                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 174
AAA22807/c
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Gaps

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0; Indels

100.0%; Prea. ...

877 CCACAAGTCCTTGT 890

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14; Conservative

Best Local Similarity Matches 14; Conserv

AAV97934 standard; RNA; 17

AAV97934;

Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence; hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;

Human BGF-R target sequence nucleotide position 5117.

(first entry)

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99WO-US06507. 98US-007967B.

```
The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl Nydrocarbon nuclear transporter (ARNY) gene, an integrin subunit beeta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17165 to AAA1768 to AAA1768 to AAA1767 to AAA1768 to AAA19677 to AAA19155 to AAA1922. represent their corresponding target sequences; AAA1768 to AAA1918 to AAA1918 to AAA1768 to AAA1768 to AAA1918 to AAA1768 to AAA1768 to AAA1818 to AAA1918 to AAA2168 to AAA1768 to AAA2168 
                                                                                                                                                                                                                                                                                                                                                                  Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        integrin subunit alpha-6, or integrin subunit beta-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 54; Page 243; 305pp; English.
                                                                                                                                                                                                                                             Pavco PA, Roberts E, Jarvis T,
                                                                                                                                                                                   (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                        WPI; 1999-591315/50.
                                                          24-MAR-1999;
                                                                                                                        27-MAR-1998;
07-0CT-1999.
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Sequence 17 BP; 0 A; 0 C; 3 G; 14 U; 0 other;

ö Length 17; Match
Local Similarity 100.0%; Pred. No. 2.5e+02;
es 14; Conservative 0; Mismatches 0; Indels Query Match Best Loca Matches

8

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AAA22808 standard; RNA; 17 BP. AAA22808;

19-JUN-2000 (first entry)

Integrin subunit beta 3 substrate sequence SEQ ID NO:6034.

Human; aryl hydrocarbon nuclear transport, ARNT; TIB-2; angiogenesis, integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antidialmantory; antidiarthritic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verruca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss

Homo gapiens.

WO9950403-A2.

17-0CT-1999.

99WO-US06507. 24-MAR-1999;

98US-0079678 27-MAR-1998;

Coeshott C, McSwiggen JA;

RIBO-) RIBOZYME PHARM INC.

Coeshott C, McSwiggen JA; Jarvie T, Pavco PA, Roberts E,

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors

Claim 54; Page 243; 305pp; English

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNY) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA1575 to AAA1761 and AAA1762 to AAA1762 represent ribozyme sequences for ARNY, corresponding target sequences, AAA1963 to AAA1963 and AAA1963 to AAA1963 to AAA1963 and AAA1963 to AAA2168 to Expresent their corresponding target sequences; AAA19623 to AAA2168 to Expresent their corresponding target sequences; AAA21689 to AAA21681 and AAA2160 to AAA2169 to AAA22169 to AAA2169 integrin subunit alpha-6, or integrin subunit beta-3.

Sequence 17 BP; 0 A; 0 C; 4 G; 13 U; 0 other;

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Gaps

ö 1.1%; Score 14; DB 1; Length 17; 100.0%; Pred. No. 2.5e+02; 0; Indels 100.0%; Pred. No. 14; Conservative Local Similarity Query Match Matches

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1207 AAACAAACAAACAA 1220

à 쉽

14 AAACAAACAACAA 1

AAA22809 Btandard; RNA; 17 BP.

RESULT 176

AAA22809;

19-JUN-2000 (first entry)

Integrin subunit beta 3 substrate sequence SEQ ID NO:6035.

Human, aryl hydrocarbon nuclear transport; ARNT; TIB-2; anglogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; anglogenic factor; cytostatic; antidiabetic; ophthalmologic; antinifiammatory; antiarthritic; antipsoriatic; ARMD;

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dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; necesscular glaucoma; myopic degeneration; psoriasis; vertuca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
                                     Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
                                                                                                                                                                                                     Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors
                                                                                                                                                                 Coeshott C, McSwiggen JA;
                                                                                                                                                                                                                                Claim 54; Page 243; 305pp; English.
                                                                                                                                                                 Jarvis T,
                                                                                                           99WO-US06507.
                                                                                                                              98US-0079678.
                                                                                                                                               (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                 Roberts E,
                                                                                                                                                                                   WPI; 1999-591315/50.
                                                                                                          24-MAR-1999;
                                                      Homo sapiens
                                                                        WO9950403-A2
                                                                                                                             27-MAR-1998;
                                                                                          07-0CT-1999,
                                                                                                                                                                  Pavco PA,
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The present invention describes enzymatic nucleus and molecules with present invention describes enzymatic nucleus and molecules with procession nuclear transporter (ARWT) gene, an integrin subunit beta 3 gene, an integrin subunit beta 3 gene, an integrin subunit beta 3 and AAA1767 and AAA1761 to AAA17621 to AAA17622 represent ribozyme sequences for ARWT, and AAA1768 and AAA1768 to AAA1868 to AAA1868 to AAA1968 to AAA2168 to present invention describes enzymatic nucleic acid molecules with integrin subunit alpha-6, or integrin subunit beta-3

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Length 17;
                                              1.1%; Score 14; DB 1; Le
100.0%; Pred. No. 2.5e+02;
tive 0; Mismatches 0;
Sequence 17 BP; 0 A; 0 C; 4 G; 13 U; 0 other;
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14; Conservative

Matches

8

Best Local Similarity

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AAA22810 standard; RNA; 17 BP
                                                           (first entry)
                                                          19-JUN-2000
                                       AAA22810;
RESULT 177
AAA22810/C
ID AAA228
XX
AC AAA228
XX
XX
XX
DF 19-JUN
XX
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Integrin subunit beta 3 substrate sequence SEQ ID NO:6036.

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; harmerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antidiafmmatory; antiarthritic; antipsoriatic; ARND; dermatological; RNN cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; poriasis; veruca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; ss. expression and/or Coeshott C, McSwiggen JA; Novel ribozymes for modulating the synthesis, expresstability of an mRNA encoding an anglogenic factors Jarvis T, 99WO-US06507 98US-0079678. (RIBO-) RIBOZYME PHARM Pavco PA, Roberts B, WPI; 1999-591315/50. 24-MAR-1999; Homo sapiens. 27-MAR-1998; WO9950403-A2

Claim 54; Page 243; 305pp; English

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an arryl hydrocarbon muclear transporter (ARNY) gene, an integrin submit beta 3 gene, an integrin submit beta 3 gene, an integrin submit beta 3 gene, and AAA1768 to AAA1768 to AAA1768 to AAA1769 to AAA1768 to AAA1768 to AAA1768 to AAA1768 to AAA1767 and AAA1168 to AAA1768 to AAA19677 to AAA1918 to Present ribozyme sequences for Tie-2, and AAA19087 to AAA1918 to AAA1763 to AAA1768 to AAA1908 to AAA1918 to AAA1763 to AAA1968 to AAA2189 integrin subunit alpha-6, or integrin subunit beta-3

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Gaps
                                                                ö
                               Length 17;
                                                                0; Indels
                             1.1%; Score 14; DB 1; L4
100.0%; Pred. No. 2.5e+02;
ive 0; Mismatches 0;
Sequence 17 BP; 1 A; 0 C; 4 G; 12 U; 0 other;
                                                 Best Local Similarity 100.
Matches 14; Conservative
                                   Query Match
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.. 0

AAA36306 standard; DNA; 17 BP 14 AAACAAACAACAA 1 RESULT 178 AAA36306 ID AAA3 XX 셤

1207 AAACAAACAAACAA 1220

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Gaps

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0; Indels

WO200192524-A2.

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A method has been developed for detecting the presence or absence of a single nuclectide polymorphism (SNP) allele in a genomic sample. The method comprises preparing a reduced complexity genome (RCG) from the genomic sample and analysing the RCG for the presence or absence of a SNP allele. The method can be used to characterise a tumour, to generate a genomic pattern for an individual genome or to generate a genomic classification code for a genome. The method can be used to assess whether a subject is at risk for developing a disease or to identify a set of SNP alleles associated with a disease. The method can also be used to perform linkage analysis. AAA35944 to AAA35947 represent sequences used in the exemplification of the present invention. AAA35948 to AAA36532 represent nucleotide sequences containing SNPs.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Detection of single mucleotide polymorphisms in genomes by preparation and analysis of reduced complexity genomes, useful for genotyping, fingerprinting and determining allele frequency of SNPs
                                                                                            Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis; allele specific oligonucleotide; ASO; reduced complexity genome; RCG; genomic classification; identification; DNA fingerprinting; tumour characterisation; hybridisation; 8s.
                                                              Kuman genomic SNP allele specific oligonucleotide SEQ ID NO:372.
                                                                                                                                                                                                                                                                                                                                            (MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                             Landers JE, Jordan B, Housman DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 64; 111pp; English.
                             26-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-293181/25.
                                                                                                                                                                                                             WO200018960-A2
                                                                                                                                                                                                                                                                                                              25-SEP-1998;
                                                                                                                                                                               нопо варіеля
                                                                                                                                                                                                                                                                             24-SEP-1999;
                                                                                                                                                                                                                                              06-APR-2000
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 AAA36306;
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Charest A;

99WO-US22283. 98US-0101757.

ö 0; Gaps Length 17; Query Match 1.1%; Score 14; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 14; Conservative 0; Mismatches 0; Indels Sequence 17 BP; 12 A; 5 C; 0 G; 0 U; 0 other;

1207 AAACAAACAAACAA 1220

1 AAACAAACAAACAA 14

ABNO7607 standard; DNA; 17 BP

Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7599.

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Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.

ABN07611 standard; DNA; 17 BP.

RESULT 180 ABN07611 ID ABN076

GCCACCATCTTACC 17

ð a

Homo sapiens

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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of bortein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 mucleic acids in samples, as amplification unbertates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific blownlecule capture probes for surface-enhanced laser desorption concentration, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polymucleotide sequences encoding hGDMLP-1 may be used for therapy. The planucleotide sequences encoding hGDMLP-1 may be used for therapy. The present and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomen used in the screening of the hGDMLP-1 sequence in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention.
N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  # Match 1.1%; Score 14; DB 1; Le Local Similarity 100.0%; Pred. No. 2.5e+02; nes 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 BP; 4 A; 7 C; 2 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published pct seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID 7599; 214pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                    30-JAN-2001; 2001W0-US00663.
30-JAN-2001; 2001W0-US00664.
30-JAN-2001; 2001W0-US00665.
30-JAN-2001; 2001W0-US00665.
30-JAN-2001; 2001W0-US00667.
30-JAN-2001; 2001W0-US00669.
30-JAN-2001; 2001W0-US00669.
30-JAN-2001; 2001W0-US00669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     myosin-like protein hGDMLP-1
                                                                                                                                                                         04-OCT-2000; 2000GB-0024263.
30-JAN-2001; 2001WO-US00661.
30-JAN-2001; 2001WO-US00662.
                                                                                                                                      2000US-234687P,
2000US-236359P.
                                                                            25-MAY-2001; 2001WO-US16981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-179446/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (AEOM-) AEOMICA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gu Y, Ji Y,
                                                                                                                                      21-SEP-2000;
27-SEP-2000;
                                  06-DEC-2001
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ABN07611;

Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss. Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7603. 21-SEP-2000; 2000US-234687P.
27-SEP-2000; 2000US-234687P.
27-SEP-2000; 2000US-23459P.
30-JAN-2001; 2001WO-US00661.
30-JAN-2001; 2001WO-US00663.
30-JAN-2001; 2001WO-US00663.
30-JAN-2001; 2001WO-US00666.
30-JAN-2001; 2001WO-US00666.
30-JAN-2001; 2001WO-US00666.
30-JAN-2001; 2001WO-US00666.
30-JAN-2001; 2001WO-US00667.
30-JAN-2001; 2001WO-US00667. 25-MAY-2001; 2001WO-US16981 WO200192524-A2 Homo sapiens 29-MAY-2002

(AEOM-) AEOMICA INC

Chen W, Rank DR, Hanzel DK, Gu Y, Ji Y, Penn SG, WPI; 2002-179446/23.

New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1

Disclosure; SEQ ID 7603; 214pp; English.

The present invention describes a human genome-derived myosin-like protein 1 (hGDWLP-1). The protein and polymucleotide sequences of hGDWLP-1 can be used in gene therapy and vaccine production. The hGDWLP-1 mucleic acids can be used as probes to detect, characterise and quantify hGDWLP-1 mucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDWLP-1 proteins. The hGDWLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDWLP-1 proteins, as standards in assays used to determine the hGDWLP-1 proteins, as specific concentration and/or amount specifically of hGDWLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption concentration and/or amount specifically of hGDWLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption confering in hGDWLP-1 production, and in vaccines or for replacement the polymucleotide sequences encoding hGDWLP-1 may be used for diagnosing a disorder associated with the expression of hGDWLP-1; in chart and skeleral muscle disorders. hGDWLP-1 in production, and disorder used in the chromosome 22. The present sequence in the exemplification of the present

invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence.

Sequence 17 BP; 3 A; 7 C; 2 G; 5 T; 0 other;

ô Gaps ö Length 17; 0; Indels Score 14; DB 1; Le Pred. No. 2.5e+02; 0; Mismatches 0; Query Match 1.1%; Scc Best Local Similarity 100.0%; Pr Matches 14; Conservative 0;

COOP 07.67.70 OT

בווני הענ

PCR primer used to amplify the human krit1 gene exon 4.

Human, krit1 gene, Ras gene, cavernoma; gene therapy, angiogenesis, vascular malformation, dysplasia; angioma; tumour; PCR primer; ss.

(INRM) INSERM INST NAT SANTE & RECH MEDICALE.

Tournier LE, Laberge Le Couteux S, Labauge P;

New primers for amplifying regions of the Kritl gene, useful for diagnosis, particularly by detecting mutations, cavernomas, and therapy with this gene

Claim 1; Page 16; 39pp; French.

PCR primers AAF24944-45 were used to amplify exon 4 of the human kriti gene. Kriti is a member of the Ras gene family. Mutations in the kriti gene are responsible for certain vascular abnormalities. The primers are used to detect mutations in the Kriti gene, specifically those mutations that are associated with presence of cavernomas, for diagnosis. The kriti gene, or its derivatives, are useful in gene therapy for controlling or inhibiting angiogenesis, e.g. in cases of vascular malformation or dysplasia, or angioma, and the Kriti protein, optionally modified, may be used similarly, particularly for treatment of tumours.

Seguence 18 BP; 0 A; 0 C; S G; 13 T; 0 other;

Gaps ö Length 18; 0; Indels 1.1%; Score 14; DB 1; Le Local Similarity 100.0%; Pred. No. 2.6e+02; hes 14; Conservative 0; Mismatches 0; Query Match Best Loc

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a

RESULT 182

BP AAQ82529/c 1D AAQ82529 standard; DNA; 20 XX AC AAQ82529; XX XX 25-WAR-2003 (updated)

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Chlamydia pneumoniae.
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                                                                                                                    04-NOV-1998;
21-NOV-1997;
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                             WO9927105-A2
                                                                                        20-NOV-1998;
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                                                            03-JUN-1999
                                                                                                                                                                                                Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monia BP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences were determined from the ends of chromosome 11-specific cosmids by automated sequencing without intermediate subcloning.

A sample of 371 DNA sequence fragments were determined and of these, 277 were suitable for STS primer prediction by computer analysis (using the "Primer" program available from E.Lander, MIT).

The STSs and crosmids were mapped by in situ hybridisation, somatic cell hybrid analysis or both. Using this method, 370 STSs specific for human chromosome 11 were generated and most of them were sequencing complex genomes, designated "sequence sampled mapping". The sequence sampled mapping method is useful for the completion of high density sequence based maps, and ultimately, for the complete sequencing of genomic DNA directly from cosmid clones.

C (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
                                                            sequence sampled mapping, genomic analysis, complex genome mapping, cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
                                                                                                                                                                                                                                                                                                                                                                                     library - by sequencing end-specific nucleotides of each clone then correlating with spatial relationship of cosmid, esp. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                        Sequencing complex genomes, present as fragments in a cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer used to amplify an ORF of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1%; Score 14; DB 1; Length 20; 100.0%; Pred. No. 2.9e+02; ive 0; Mismatches 0; Indels
                                  Chromosome 11 (locus CALCA) STS primer CALCA-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                 (SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page 86; 128pp; English
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                                                                                                                                                                                                                                    93US-0078471.
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   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                           nammalian chromosomes.
                                                                                                                                                                                                                                                                                                                                            WPI; 1995-036508/05.
                                                                                                                                           W09429486-A1
                                                                                                                                                                                                       15-JUN-1994;
                                                                                                                                                                                                                                    15-JUN-1993;
                                                                                                                                                                                                                                                 07-SEP-1993;
   13-SEP-1995
                                                                                                                                                                       22-DEC-1994
                                                                                                              Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches

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AAX91991-X97517 represent PCR primers used to amplify open reading frames and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent by the open reading frames of the C. pneumoniae genome (see AAX94584-AAX95879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae muclectides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitogen-activated protein kinase; MAPK; MAPK kinase 6; antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human MAPK kinase 6 inhibiting antisense oligo ISIS# 101530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14; DB 1; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 other;
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                                                                                                                                                                                                                                                                                                 Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                      Page 1827; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB
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98WO-IB01890
                                                    98US-0107078,
97FR-0014673.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
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Novel antisense oligonucleotides used for inhibition of
Mitogen-activated protein kinase kinase 6 expression
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Example 15; Column 41; 33pp; English.

The invention provides antisense oligonucleotides which are targeted to an unclaid acid encoding a mitogen-activated protein kinase (MPAE) kinase 6. The antisense oligonucleotides are used to inhibit MAPK kinase expression, and so are used to treat diseases mediated by MAPK kinase 6 expression. They may also be used to detect MAPK kinase 6, e.g. in sandwich assays. Sequences AA289558-597 represent antisense oligos inhibiting human MAPK kinase 6 mRWA.

Sequence 20 BP; 15 A; 3 C; 2 G; 0 U; 0 other;

Gaps ö 1.1%; Score 14; DB 1; Length 20; Similarity 100.0%; Pred. No. 2.9e+02; 14; Conservative 0; Mismatches 0; Indels Matches 14; Conservative Query Match Local

1207 AAACAAACAAACAA 1220 7 AAACAAACAAACAA 20 ઠે

RESULT 185

AAS13722/c ID AAS13722 standard; DNA; 20 (first entry) 08-MAY-2002 AAS13722;

Simple sequence repeat, SSR, #19

Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.

Poeae.

NZ509193-A.

25-MAY-2001,

03-JAN-2001; 2001NZ-0509193

24-DEC-1999; 99AU-0004906. 04-MAY-2000; 2000AU-0007310.

(SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R. UNIV SOUTHERN CROSS. STATE VICTORIA DEPT NATURAL RES & ENVIRO.

UNIV ADELAIDE (UXAD-)

INT MAIZE & WHEAT IMPROVEMENT CENT. (ITMB-)

Forster JW, Jones ES;

WPI; 2001-512563/56.

New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species varieties

Claim 6; Page 51; 72pp; English.

The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2-6 nucleotides in length. Also included are a nucleic acid primer suitable for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and identifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for selecting for fescue genomic DNA enriched for SSRs prepared by the M1, selecting for

a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profilling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal seed batches by assessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal sheeding, for profilling grass or cereal species varieties, for testing the purity of grass or cereal seed batches, and for DNA profilling to establish the distinct identity, uniformity and/or stability of a cultivar. The present sequence is a ryegrass or fescue SSR.

8888888888888

Sequence 20 BP; 0 A; 0 C; 5 G; 15 T; 0 other;

Gape ő 1.1%; Score 14; DB 1; Length 20; 100.0%; Pred. No. 2.9e+02; tive 0; Mismatches 0; Indels 14; Conservative Best Local Similarity Query Match Matches

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ठे 셤 RESULT 186 ABZ01980/c

ABZ01980 standard; DNA; 50 BP.

ABZ01980;

(first entry) 09-JAN-2003 Human leukocyte gene expression profiling probe SEQ ID NO 1971.

17; leukocyte, gene expression profiling, allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, cytomegalovirus, infection,

Homo sapiene.

WO200257414-A2.

25-JUL-2002.

22-OCT-2001; 2001WO-US47856.

20-OCT-2000; 2000US-241994P.

(BIOC-) BIOCARDIA INC.

Fry K, Matcuk G, Altman P, Prentice J, Phillips J; d R, Quertermous T, Johnson F; Ly N, Woodward R, Wohlgemuth J,

WPI; 2002-636525/68.

New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides

Claim 1; Page 389; 2038pp; English.

The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, then allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus,

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Solanidine; glucosyltransferase; potato; citrate synthase; target; hammerhead ribozyme; hairpin ribozyme; alkaloid biosynthesis; flower formation; cleavage; solanaceous plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                               New enzymatic nucleic acid(s) - useful for, e.g. reducing alkaloid biosynthesis or regulating flowering
                                                                                                      Potato citrate synthase target sequence position 1333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 53; Page 56; 79pp; English.
                        AAV96639 standard; RNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                    (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                             McSwiggen JA, Zwick MG;
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-427939/36.
                                                                                                                                                                                       Solanum tuberosum.
                                                                                                                                                                                                                 WO9832843-A2
                                                                                                                                                                                                                                                                      14-JAN-1998;
                                                                                                                                                                                                                                                                                                24-NOV-1997;
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28-JAN-1997;
                                                                            01-MAR-1999
                                                                                                                                                                                                                                            30-JUL-1998
                                                     AAV96639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
RESULT 188
           AAV96639
                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents the preferred target sequence for an enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves the human c-myb sequence at the base position indicated in the descriptor line. The c-myb sequence was screened for optimal ribozyme target sites using a computer folding algorithm, and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme cleavage sites were identified. Ribozymes were synthesised and their activities optimised by either varying the length of the binding arms or by modification to prevent degradation by nucleases. The ribozymes cleave the c-myb sequence and can be used to prevent smooth muscle cell hyperproliferation in restenosis, especially after coronary angioplasty, and in cancers.
                                                                                Gaps
                                                                                                                                                                                                                                                                                   Human c-myb hammerhead ribozyme target sequence (nt. position 2713).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New enzymatic nucleic acid molecules - which cleave RNA produced by e.g. c-myb, for treating restenosis or cancer
rheumatoid arthritis, osteoarthritis or cytomegalovirus infection.
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                                                                                                                                                                                                                                                                                                            Enzymatic nucleic acid; hammerhead; ribozyme; cleavage; human; smooth muscle cell; hyperproliferation; restenosis; cancer; c-myb; coronary angioplasty; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
1.1%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indel8
                                                   Length 50;
                                                                               0; Mismatches 15; Indels
                                                                                                          1079 GCAAGAATTTGGAAAATAGAAGATGAATCATTGATTG 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Draper K, Jarvis T, McSwiggen J, Stinchcomb DT;
                                                                                                                                   42 GCAAGAATTACTAATATTGACTGTGGAGTTTTGGCTG 5
                                                     Score 14; DB 1;
Pred. No. 4.6e+02;
                            Seguence 50 BP; 19 A; 10 C; 7 G; 14 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 77; 128pp; English.
                                                      1.1%;
                                                                                                                                                                                                        AAT81506 standard; RNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0373124.
94US-0245466.
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                                                                                                                                                                                                                                                            (first entry)
                                                   Query Match
Best Local Similarity 60.5
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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18-MAY-1994;
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97US-0936545. 97US-0036545. 97US-0036599.

98WO-US00738.

(first entry)

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The present invention describes enzymatic nucleic acid molecules with RNA-cleaving activity (e.g. ribozymes) which are capable of modulating the expression of plant genes: (i) involved in biosynthesis of AAV96334, and AAV96335 to AAV96335 to AAV96335 to AAV96335 to AAV96335 to AAV963569 to AAV96331, and AAV96355 to AAV963569 to AAV963981, and AAV96355 to AAV96734 represent potato solanidine glucosyltransferase target sequences. AAV9673 to AAV97170, and AAV97171 to AAV97195 to Experesent potato citrate synthase hammerhead and halriph ribozymes. respectively. AAV96735 to AAV97772, and AAV97719 to AAV97195 cortato citrate synthase hammerhead and halriph in inozymes. respectively. AAV96735 to AAV96773, and AAV97719 to AAV97720 represent potato citrate synthase synthesis of the present cortato and be used to inhibit the synthesis of toxic alkaloids in incortants, particularly potato but also tomato, pepper. and citrate synthase is of toxic alkaloids in cabergine and ditura or to inhibit flowering in potato, lettuce, spinach, cabergine and ditura or to inhibit flowering in potato, lettuce, spinach, cabergine and turf grass. Also the ribozymes can be used for RNA manipulation in the same way that restriction endonucleases are for DNA, as well as to examine genetic drift and mutations in plants and to consenus sequences within a family of related genes, and being to catalytic need to be present at only very low concentrations.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 6 A; 1 C; 3 G; 7 U; 0 other;
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ID AAA19037 standard; RNA; 17 BP.
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Gaps

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1615 TTAAATATATATIGIT 1631

17 TAAAATATAATTTTT

schultz143-3.rng

AAA19037;

19-JUN-2000 (first entry)

Human TIE-2 substrate sequence SEQ ID NO:2263.

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; harmmerhaad ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antidilamalory; antiarthritic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verucea vulgaris; angiofibroma; tuberous sclerosis; poct-wine stain; Sturge Weber syndrome; Ss.

Homo sapiens.

WO9950403-A2

07-OCT-1999.

99WO-US06507. 4-MAR-1999; 98US-0079678. 27-MAR-1998;

(RIBO-) RIBOZYME PHARM INC.

Coeshott C, McSwiggen JA; Jarvie T, Pavco PA, Roberts B,

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an anglogenic factors

Claim 56; Page 132; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl Phydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, and AAA17167 and AAA17167 to AAA17167 and AAA17621 to AAA17621 to AAA17684 tepresent their corresponding target sequences; AAA17685 to AAA18385 and AAA19086 to AAA19154 represent ribozyme sequences for Tie-2, and AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA19087 to AAA19223 represent their corresponding target sequences; AAA19223 to AAA19222 represent their corresponding target sequences; AAA19223 to AAA19222 represent their corresponding target sequences; AAA19225 to AAA21688 represent their corresponding target sequences; AAA21689 to AAA21685 and AAA21685 represent their corresponding target sequences; AAA21689 to AAA21689 to AAA21689 to AAA21689 to AAA21689 to AAA21689 represent their corresponding target sequences; Cfor integrin subunit beta 3, and AAA22476 to AAA23262, AAA23333 to the invention are used for modulating the synthesia sequences; creability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit beta 3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARND), inflammation, and atthritis, as well as macular degeneration (ARND), inflammation, and atthritis, werder ungarias; cancer diabetic retinopathy, escape related to the levels of ARNT, Tie-2, integrin shumit allaha-6, or the levels of ARNT, Tie-2, integrin shumit allaha-6, or integrin syndrome, syndrome, syndrome, syndrome integrin subunit alpha-6, or integrin subunit beta-3.

Sequence 17 BP; 4 A; 1 C; 2 G; 10 U; 0 other;

ö 1.1%; Score 13.8; DB 1; Length 17; 18.2%; Pred. No. 2.7e+02; ve 0; Mismatches 2; Indels 1590 AAATATAAAAGTAAATA 1606 88.2%; Query Match
Best Local Similarity 88.2°

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Gaps

AAA21468 standard; RNA; 17 BP RESULT 190 AAA21468,

AAA21468;

(first entry) 19-JUN-2000

Integrin alpha 6 subunit substrate sequence SEQ ID NO:4694.

Human; aryl hydrocarbon nuclear transport; ARNT; TIB-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; harmerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; autiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovaecular glaucoma; myopic degeneration; psoriasis; vertuca vulgaris; angiofibroma; tuberous solerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens.

W09950403-A2.

07-OCT-1999.

99WO-US06507. 24-MAR-1999;

(RIBO-) RIBOZYME PHARM INC.

98US-0079678.

27-MAR-1998;

Jarvis T, Coeshott C, McSwiggen JA; Pavco PA, Roberts E,

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors

Claim 55; Page 210; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl RNA cleaving activity, which specifically cleave RNA encoded by an aryl or phydrocarbon nuclear transporter (ARNY) gene, an integrin subunit beta 3 gene, and AAA17651 to AAA17622 represent ribozyme sequences for AAA1765 and AAA17635 to AAA1868 represent their corresponding target sequences; AAA17635 to AAA1868 represent their corresponding target sequences; AAA1955 to AAA1968 and AAA1908 to AAA1908 corresponding target sequences; AAA1915 to AAA1915 to AAA1915 to AAA1915 to AAA1916 to AAA2160 to AAA21501 to AAA21505 to AAA1908 target sequences; AAA1915 to AAA2168 to AAA2316 t .ntegrin subunit alpha-6, or integrin subunit beta-3.

Sequence 17 BP; 9 A; 0 C; 0 G; 8 U; 0 other;

Length 17; Score 13.8; DB 1; Pred. No. 2,7e+02; 1.1%; Query Match Best Local Similarity

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AAATATACAAGTCAATA

17

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Gaps

.. 0

Indels .. 73 0; Mismatches 1133 TTATAGTAAATTTATTT 1149 17 TTATAAAAATTTATT 1 15; Conservative Matches ઠે 윱

AAA21475 standard; RNA; 17

AAA21475

(first entry) 19-JUN-2000

Integrin alpha 6 subunit substrate sequence SEQ ID NO:4701.

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; harmeread ribozyme; andiogenic factor; cytostatic; antidabetic; ophthalmologic; antidiamatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; vertuca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens.

WO9950403-A2

07-0CT-1999.

99WO-US06507 24-MAR-1999;

98US-0079678 27-MAR-1998;

(RIBO-) RIBOZYMB PHARM INC.

Coeshott C, McSwiggen JA; Pavco PA, Roberts E, Jarvis T,

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors

Claim 55; Page 210; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl Widractory man an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a fie-2 gene. AAA16775 Lo AAA1762 to AAA1762 to AAA1763 to AAA1762 to AAA1763 to AAA1764 represent their corresponding target sequences; Corresponding target sequences; AAA1915 to AAA1915 and AAA2195 to AAA2196 to

ö Gaps ö Length 17; Integrin subunit beta 3 substrate sequence SEQ ID NO:6130. Indels Score 13.8; DB 1; Pred. No. 2.7e+02; 0; Mismatches 2; Sequence 17 BP; 5 A; 1 C; 3 G; 8 U; 0 other; 555 AAA22904 standard; RNA; 17 BP 3.14; 539 AAACAATGAATAGTTTT 17 AAACAATGAACACTTTT 19-JUN-2000 (first entry) Query Match Best Local Similarity 88.2 Matches 15; Conservative AAA22904; RESULT 192 AAA22904/ Ġ g

Human; aryl hydrocarbon nuclear transport; ARNT; TIB-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; harmenead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verruea vulgaris; angiofibroma; tuberous scleroais; pot-wine stain; Sturge Weber syndrome; Rippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens #09950403-A2

07-OCT-1999.

24-MAR-1999;

99WO-US06507.

98US-0079678. 27-MAR-1998; (RIBO-) RIBOZYME PHARM INC.

Pavco PA, Roberts B, Jarvis T, Coeshott C, McSwiggen JA;

WPI; 1999-591315/50.

expression and/or Novel ribozymes for modulating the synthesis, expresstability of an mRNA encoding an angiogenic factors

Claim 54; Page 249; 305pp; English.

RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 can by decarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 can by a carbon and AAA1765 to AAA1765 to AAA1765 to AAA1765 to AAA1765 to AAA1768 to AAA1768 to AAA1765 to AAA1768 to AAA1768 to AAA1766 to AAA1768 to AAA1766 to AAA1168 to AAA1766 to AAA1168 to AAA1169 to AA The present invention describes enzymatic nucleic acid molecules with

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A method has been developed for the identification of a nucleic acid capable of modulating a process in a biological system. The method comprises: (a) introducing into the system a random library of nucleic acid catalysts (NAC) having a substrate binding domain (SBD), comprising a random sequence, and a catalytic domain (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDs in such systems. Nucleic acid molecules with endonuclease activity and catalytic activity, from the present
     vulgaria,
neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2, integrin subunit alpha-6, or integrin subunit beta-3.
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme; target; substrate; catalyst; modulation; expression; Raf gene; delivery; screening; identification; synthesis; deprotection; purification; poriasis; non-hepatic ascites; infection; genetic drift; restenosis; rheumatoid arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, restencis, and also new ribozymes and modified nucleoside triphosphates used as antiviral agents and synthons
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                                                                                                                                     1.1%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 2.7e+02; ive 0; Mismatches 2; Indels
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Karpeisky A, Kisich K, Matulic-Adamic J, McSwiggen JA,
Parry T, Reynolds M, Sweedler D, Thompson J, Workman
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human C-raf target site nucleotide position 2967.
                                                                                                     Sequence 17 BP; 12 A; 0 C; 0 G; 5 U; 0 other;
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970S-0049002.
970S-0051718.
970S-0056808.
970S-0061321.
970S-0061324.
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                                                                                                                                                                                                                                                                                                                                  AAV91422 standard; RNA; 17
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                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                   Query Match 1.1
Best Local Similarity 88.2
Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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02-OCT-1997;
02-OCT-1997;
05-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                     AAV91422;
                                                                                                                                                                                                                                                                                                   RESULT 193
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invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases caused by specific RNA. e.g. ancer, inflammation, psoriasis, non-hepatic ascites and infection. They may also be used to detect genetic drift and mutations in diseased cells and to determine expression of the Raf gene, are used to treat cancer, restencesis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of c-raf. Introduction of sugar/phosphate modifications increases stability against nuclease and activity. AAV90922 to AAV93877 represent NACs that can be used in the method, specifically for modulating the expression of a Raf gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of represor genes encoding the TR2 Orphan receptor. EARJ/COUP-TF-1, the GATA transcription factor gene, TRR-2 and/or the CAAT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha.
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enzymatic and antisense mucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.
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                                                                                                                                                                                                                                                                                 Length 17;
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                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                               1.1%; Score 13.8; DB 1;
88.2%; Pred. No. 2.7e+02;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                               Sequence 17 BP; 12 A; 0 C; 0 G; 5 U; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McSwiggen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hammerhead ribozyme substrate #721.
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                                                                                                                                                                                                                                                                                                                                                           1137 AGTAAATTEATTITATT 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APR-2000; 2000WO-US09721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0129390.
                                                                                                                                                                                                                                                                                                                                                                            17 ATTTATTTATTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF02426 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                    Local Similarity 88.2
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-647423/62.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-FBB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF02426;
                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                        Best Local
Matches
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1 AAAAGITFITAIGIGC 17

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with a target sequence and contain at least one phosphoro(di)thicate link, having endounclease activity. (A), and more generally any catalytic mucleic acid (A*) that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or receptor gene, are used to treat cancer (particularly of breast or reated cells, or for other conditions sesociated with levels of cestrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with also be used to correlate inhibition of gene expression with cargets, and as research reagents (for RNA, in the same way that targets, and as research reagents (for RNA, in the same way that restriction endomucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases binding affinity and/or activity. AAA21503 to AAA21477 represent oestrogen receptor hammerhead ribozyme sequences, and AAA21610 to AAA2610 represent corresponding target sequences, and AAA2610; to AAA2611 represent cetrogen receptor hairpin ribozyme sequences. AAA28219 to AAA2611 represent other ribozyme sequences and antisense oligonucleotides used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention describes nucleic acids (A) that interact stably
                                                                                                                                                                                                                                                      Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1862
                                                                                                                                                                                                                                                                                          Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; harmerhead ribozyme; bairpin ribozyme; antisense oligonuclectide; pagene expression modification; cancer; phosphorothicate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acids that interact, and optionally cleave, target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 6 A; 1 C; 3 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thompson JD, Beigelman L, McSwiggen JA, Reynolds M, Zwick M, Jarvis T, Woolf T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 77; Page 77; 148pp; English.
1204 ATTAAACAAACAA 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences, used to treat cancer
                                                                                                                                   AAA25364 standard; DNA; 17 BP
                                 17 ATTATACATACAACAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US08547,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0082404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                               19-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-013248/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matulic-Adamic J;
                                                                                                                                                                                                                                                                                                                                                                                                                                    W09954459-A2.
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-APR-1999;
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                                                                                                                                                                         AAA25364;
                                                                                            RESULT 195
                                                                                                                AAA25364
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Bellon L;

Karpeisky A, Haeberli P;

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The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro (di)thioate link, having endowuclease activity. (A), and more generally any catalytic nucleic acid (A) that modulates expression of the cestrogen receptor gene, are used to treat cancer (particularly of breast or receptor gene, are used to treat cancer (particularly of breast or receptor gene, are used to treat secondated with levels of treated cells, or for other conditions associated with levels of can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity, AAA23503 to AAA24747 represent centrogen receptor hairboryme sequences, and AAA2593 to AAA2592 represent their corresponding target sequences, and AAA25919 to AAA2592 represent their excresponding target sequences, and AAA25919 to AAA2592 represent their corresponding target sequences, and AAA25919 to AAA2592 represent their corresponding target sequences, and AAA25919 to AAA2592 represent their corresponding target sequences, and AAA25919 to AAA2592 represent their corresponding target sequences. AAA25919 to AAA25921 represent their corresponding target sequences. AAA25919 to AAA25921 represent other their corresponding tearget sequences. AAA25919 to AAA25921 represent their corresponding tearget sequences and adaptisents of in the
                                                                                                                                                                              Jestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1865.
                                                                                                                                                                                                                     Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; thairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothicate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bellon L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 2.7e+02; ve 0; Mismatches 2; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beigelman L, McSwiggen JA, Karpeisky A,
Zwick M, Jarvis T, Woolf T, Haeberli P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 4 A; 2 C; 3 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other ribozyme sequences and antisense olexemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 77; Page 77; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1541 ATGITTITATGIGCICT 1557
                                           AAA25367 standard; DNA; 17 BP
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                                                                                                                                 (first entry)
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Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matulic-Adamic J;
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Reynolds M,
                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                      AAA25367;
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RESULT 196
                     AAA253
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1 AAGTTTTTATGTGCACT

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1.1%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 2.7e+02; ve 0; Mismatches 2; Indels

Query Match 1.1%; Best Local Similarity 88.2%; Matches 15; Conservative

Human, gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.

28-JAN-2002; 2002EP-0001167.

07-AUG-2002

Homo sapiens. EP1229046-A2. 30-JAN-2001; 2001WO-US00667. 30-JAN-2001; 2001WO-US00668. 30-JAN-2001; 2001WO-US00668. 323-MAX-2001; 2001WS-0864761. 09-OCT-2001; 2001US-0327898.

30-JAN-2001; 30-JAN-2001; 30-JAN-2001;

Human HTPL scanning oligonucleotide SEQ ID 1930.

(first entry)

03-JAN-2003

ABV80684;

ABV80684 standard; DNA; 17 BP.

ABV80684,

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Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2488
                                                                      Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; ribozyme; antisense oligonucleotide; hammerhead ribozyme; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.
                                                                                                                                                                                                                                         McSwiggen JA, Karpeisky A, Bellon L;
is T, Woolf T, Haeberli P;
                                                                                                                                                                                                                                                                                                New nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer
                                                                                                                                                                                                                                                                                                                           Claim 77; Page 97; 148pp; English.
                                                                                                                                                                                                                                        Thompson JD, Beigelman L, McSwir
Reynolds M, Zwick M, Jarvis T,
AAA25990 standard; DNA; 17 BP.
                                                                                                                                                                                            98US-0082404.
98US-0103636.
                                                                                                                                                                          99WO-US08547.
                                                                                                                                                                                                                       RIBO-) RIBOZYME PHARM INC.
                                  (first entry)
                                                                                                                                                                                                                                                                             WPI; 2000-013248/01.
                                                                                                                                                                                                                                                             Matulic-Adamic J;
                                                                                                                                      WO9954459-A2.
                                  19-JUL-2000
                                                                                                                                                                           19-APR-1999;
                                                                                                                    Hono sapiens
                                                                                                                                                                                             20-APR-1998;
                                                                                                                                                                                                       23-JUN-1998;
                                                                                                                                                        28-OCT-1999
                AAA25990;
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The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thioate link, having endomiclase activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the cestrogen receptor gene, are used to treat cancer (particularly of breast or reated cells, or for other conditions associated with levels of cestrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with a laterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that a restriction endomucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24747 represent oestrogen receptor harmerhead riboxyme sequences, and AAA26103 to AAA2618 represent cereptor harmpin riboxyme sequences, and AAA26107 to AAA2618 represent cereptor their corresponding target sequences, and AAA26107 to AAA2618 represent cereptor their corresponding target sequences, and AAA26107 to AAA2618 represent cereptor their corresponding target sequences, and AAA26107 to AAA2618 represent cereptor their corresponding target sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      other ribozyme sequences and antisense ol exemplification of the present invention.
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Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL -

WPI; 2002-676582/73.

Zhan J;

(AEOM-) AEOMICA INC.

Example 2; Page 316; 718pp; English.

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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL chas two isoforms, with a few single base pair differences between the two isoforms, with a few single base pair differences between the two of the single base pair changes introduces a premature stop codon in HTPL-8 (8 for short) compared to HTPL-1 (1 for long). HTPL canners an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was important in regulating male germ cell development, and the HTPL, and in therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of the HTPL. Such disorders include disorders expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foctal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from. the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.1%; Score 13.8; DB 1; Length 17;
18.2%; Pred. No. 2.7e+02;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 6 A; 3 C; 2 G; 6 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 BP; 7 A; 1 C; 2 G; 7 T; 0 other;
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Local Similarity 88.2 les 15; Conservative

Query Match Matches ABZ61055

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Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
                                                                                                                                                                                                                                                                                                                                                                                 Bnzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma
                                                                                                                                                                                                                                                                                                                           Szymkowski DE
                                                                                                                                                                                                                                                                                                                          Thompson J, McSwiggen J, McKenzie T, Ayers D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzymatic nucleic acid molecule of the invention
                                                                   Human CLCA1 gene enzymatic nucleic acid #1862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17 BP; 6 A; 1 C; 1 G; 9 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 114; 152pp; English.
ABK57491 standard; RNA; 17 BP
                                                                                                                                                                                                                                                        09-AUG-2000; 2000US-224383P.
                                                                                                                                                                                                                                 09-AUG-2001; 2001WO-US24970.
                                                                                                                                                                                                                                                                            (RIBO-) RIBOZYME PHARM INC.
(SYNT ) SYNTEX USA LLC.
(THOM/) THOMPSON J.
                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-217145/27.
                                                                                                                                                                                    WO200211674-A2.
                                                                                                                                        acetylcysteine
                                                                                                                                                              Homo sapiens.
                                             02-JUL-2002
                                                                                                                                                                                                          14-FEB-2002.
                       ABK57491;
                                                                                                                                                                                                                                                                                                                                       Grupe A;
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The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes conjusted from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapy bronchodilators conticosteroids, the use of one or more therapy bronchodilators corticosteroids, antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1, RNA in a cell. This sequence represents an
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ö Gaps ö Query Match 1.1%; Score 13.8; DB 1; Length 17; Best Local Similarity 35.3%; Pred. No. 2.7e+02; Matches 6; Conservative 9; Mismatches 2; Indels

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RESULT 200

The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytostatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The mucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ65216, ABZ64544 - ABZ65531, ABZ6520 - ABZ65216, ABZ65530 - ABZ6530 - ABZ65530 - ABZ65 Novel short interfering RNA and enzymatic nucleic acid useful for treating cancer, wodulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences Gaps A. thaliana plant morphogenesis regulatory protein RT-PCR primer. Human, ribozyme, short interfering RNA; siRNA; HER2; K-Ras; enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV; anti-rheumatic; cancer; AIDS; ss. ö Plant; morphogenesis; regulation; short; stem; alteration; inflorescence; extraneous; gene; expression; transformation; 1.1%; Score 13.8; DB 1; Length 17; 58.8%; Pred. No. 2.7e+02; tive 5; Mismatches 2; Indels Sequence 17 BP; 10 A; 2 C; 0 G; 5 U; 0 other; Human K-Ras DNAzyme substrate #1167. Claim 58; Page 107; 185pp; English. 1605 TATGAARCATTTAAAAT 1621 ABZ61055 standard; RNA; 17 BP. 1 UAUCAAACAUUAAAAAU 17 AAT62126 standard; DNA; 18 BP 29-MAY-2002; 2002WO-US16840. 29-MAY-2001; 2001US-294140P. 06-JUN-2001; 2001US-296249P. 10-SEP-2001; 2001US-318471P. (RIBO-) RIBOZYME PHARM INC. 10-JUN-1997 (first entry) 10; Conservative WPI; 2003-140484/13. Local Similarity WO200297114-A2. Homo Bapiens. 21-MAR-2003 05-DEC-2002. Mcswiggen J; AAT62126; Query Match Best Loca Matches RESULT 201 **AAT**62126, 8 쉽 244444444 24444444

schultz143-3.rng

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WPI; 1998-286974/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                 AAV17951;
                                                                                                                                                                                                                                                                                                                                                                            RESULT 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; primer; ss.
                                                                                                                                                                                                                     The present sequence is a RT-PCR primer for a mRNA encoding an Arabidopsis thaliana plant morphogenesis regulatory protein (MRP), which can be used to yield a plant with, e.g. short stems or altered inflorescence. The MRP acts on a plant at a specific site for a specific period, and can therefore be used to regulate extraneous gene expression in a plant. The MRP's cDNA or genomic DNA can be used to transform a plant to increase its MRP expression, and therefore control the form (particularly stem length) of the plant.
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                                                                                                                                                                        DNA encoding plant morphogenesis regulatory protein - useful yield plants with short stems or altered inflorescence
                                                                                                                                                                                                                                                                                                                                       1.1%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 2.9e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human biallelic polymorphic marker upstream primer #339
  increase, control, form; length, primer; RT-PCR, reverse transcriptase; polymerase chain reaction; ss.
                                                                                                                          (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
(CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU.
                                                                                                                                                                                                                                                                                                                     Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 other;
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                                                                                                                                                                                                     Example; Page 15; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                              1498 GACTGCATTTTAAATA 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang D;
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                                                                                                        95JP-0216187
                                                                                                                                                                                                                                                                                                                                                                                           11 GACTGCGTTTTTAGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX09459 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Best Local Similarity 88.2
Matches 15, Conservative
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                                                                                                                                                       WPI; 1997-206629/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                        24-AUG-1995;
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                                                  JP09056382-A
                                                                                      24-AUG-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                              Synthetic.
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AXX09121-X10268 are allele-specific cligonuclectide primers used in the isolation of various biallelic polymorphic markers found in the human genome (represented in AAX10269-X1293). These primers can be used in a method for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidual, Lesch-Nyhan syndrome, con use and as agammaglobulinemia, diabetes insipidual, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Pabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, you Willebrand's disease, thereditary spherocytosis, you Willebrand's disease, thereditary syndrome, osteogenesis imperfecta, acute intermittent porphyria, autorimmune diseases, inflammation, cancer, diseases of the nervous syndrome, osteogenesis inflammation, cancer, diseases of the nervous as longerity, appearance (e.g. baldness, obesity), strength, speed, as longerity, and susceptibility or receptivity to particular dungs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or prophylaxis of such diseases.
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New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 2.9e+02; varive 0; Mismatches 2; Indels
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                                                                                                                                                                             Claim 15; Page 93; 310pp; English
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Best Local Similarity 88.2
Matches 15, Conservative
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The any of the same time without losing its sensitivity and specificity. This at the same time without losing its sensitivity and specificity. This at the same time without losing its sensitivity and specificity. This is and and possible by the usage of three 16s IRRN species specific primers pairs (AAV17953-V17956). The optional first step subjects the test sample to a PCR reaction which uses the Chlamydia genus specific 16s IRNA sense and antisense (AAV17952) primers to amplify the generic 16s IRNA sense and antisense (AAV17952) primers to amplify the generic 16s IRNA sense and antisense (AAV17952) primers to amplify the generic 16s IRNA subjected to another PCR reaction with the species specific primers. The type of Chlamydia species present is indicated by the length of the PCR product. A 412 bp product would indicate C. pneumoniae and a 127 bp product would indicate C. pneumoniae and a 127 bp product would indicate C. pneumoniae and a 127 bp product would indicate C. psittaci. These primers can also the used as species specific probes. The assay can be used to equally identify e.g. C. trachomatis from endocervical swab samples, C. psittaci from cloacal swab samples from birds and C. pneumoniae from sputum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel biallelic markers used to construct a high density disequilibrium
             invention provides a novel assay for detecting and differentiating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human biallelic marker downstream amplification primer SBQ ID NO:9394.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome, biallelic marker; high density disequilibrium map, genomic map, haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
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                                                                                                                                                                                                                                                                                                                                                                           Score 13.8; DB 1; Length 18;
Pred. No. 2.9e+02;
0; Mismatches 2; Indels
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                          samples
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AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ7440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density

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mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other
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88.2%; Pred. No. 2,9e+02;
ive 0; Mismatches 2; Indels
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Best Local Similarity
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                                                                                                                                               treatment.
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BP.

(first entry)

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Human; glutamate carboxypeptidase II; GCPII gene; dietary folate; FGCP; folypoly-gamma-glutamate carboxypeptidase; hyperhomocyteinaemia; cardiovascular disease; Alzheimer's disease; neural tube defect; congenital heart defect; colon cancer; FCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                     Screening an individual for increased risk of low folate status, comprises detecting mutation in human glutamate carboxypeptidase II gene which affects ability of hydrolyzing terminal glutamates from
                                                                     Human GCPII gene exon-4 amplifying PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Page 26; 38pp; English.
                                                                                                                                                                                                                                              12-MAR-2001; 2001WO-US07880.
                                                                                                                                                                                                                                                                      13-MAR-2000; 2000US-0188983
AAD17639 standard; DNA; 18
                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                   Homo sapiens
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                          AAD17639;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoing a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1
                                                                                                                    Gaps
    treatment.
N.B. The SEQ ID NOB 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
and 3367, are not actually given a sequence in the Sequence Listing
from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 2.9e+02; ive 0; Mismatches 2; Indels
                                                                                          Length 18;
                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                           Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
                                                                                                                                                                                                                                                                                                                 Cdc 2 kinase hammerhead ribozyme recognitoin site #37.
                                                                                     1.1%; Score 13.8; DB 1;
ilarity 88.2%; Pred. No. 2.9e+02;
Conservative 0; Mismatches 2;
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                                                                 Seguence 18 BP; 0 A; 6 C; 3 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barber JR, Robbins JM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 18; 109pp; English
                                                                                                                                              895 CIGIGCCTIGGTTTCEC 911
                                                                                                                                                         2 CTGFGCCTTGFCTTCTC 18
                                                                                                                                                                                                                             .606/c
AAA86606 standard; DNA; 18 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US28772.
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                                                                                                                                                                                                                                                                                          04-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tritz R, Welch PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMMU-) IMMUSOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-412314/35
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Best Local Similarity
                                                                                                   Local Similarity
ses 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                            restenosis; ss
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                                                                                                                                                                                                                                                                                                                                                                                   Mammalia.
                                                                                                                                                                                                                                                                AAAB6606;
                                                                                           Query Match
                                                                                                                                                                                                              RESULT 206
                                                                                                                    Matches
                                                                                                                                                                                                                             AAAB6606,
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Devlin AM;

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The patent discloses methods for screening an individual for increased risk of low folate status. The method involves detecting a mutation in the human glutamate carboxypeptidase (GCP) II gene in a biological sample from said individual, wherein detection of the mutation is indicative of decreased ability of an individual to hydrolyge terminal glutamate residues from dietary folates by folypoly-gamma-glutamate carboxypeptidase (FGCP), a product of GCPII gene. The decreased ability is associated with low folate status. The method is useful for screening an individual for increased risk of low folate status and conditions cancer and altered cognition in the elderly including Alzheimer's disease. Pregnant women with low folate status are at increased risk of bearing children with neural tube defects and congenital heart defects. The primer which is used for amplifying exon-4 of GCPII gene. This primer is designed from PSWA amplifying exon-4 of GCPII gene. This primer is designed from PSWA genomic sequence and is used for detecting a mutation in GCPII gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 2.9e+02; ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 18 BP; 2 A; 2 C; 3 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        767 GCATCACATAAAATGA 783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH61772 standard; DNA; 18
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see 15, Conserv
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AC AAI
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TTTATTAGATAAATTTC 1188

1172

Conservative

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Matches

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RESULT 207 AAD17639/c

Haematopoietic cell proliferation disorder related oligonucleotide #735.

(first entry)

16-JAN-2003

Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; probe; primer; ss.

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The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme [1] which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinse (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promote poperably linked to a nucleic acid segment encoding [1]. (I) can have antipsoriatic, dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling, ophthalmological, vytostatic, acidical and virucide activities, and cleaves RNA encoding (II) and have useful for treating proliferative cleaves RNA encoding cytokine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, squamous or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and rectinal detachment, and for treating and preventing prematuring scarr. AAHS1577 to AAH62099 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
Human, ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnerary; proliferative disease; skin disease; skin disease; skin disease; skin disease; skin disease; cyclinis diabetic retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP; antipsoriatic; dermatological; artiseborrheic; antidiabetic; virucide; antistokling; ophthalmological; artiseborrheic; antidiabetic; virucide; antistokling; ophthalmological; keratolytic; gene therapy; viral wart; atopic dermatitis; actinic keratosis; squamous cell carcinoma; basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar; sickle cell retinopathy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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18.2%; Pred. No. 2.9e+02;
Ive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 378; 408pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robbins JM, Tritz R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMU-) IMMUSOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-300427/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG

WPI; 2003-018942/01.

Claim 15; Page 52; 117pp; English.

dinucleotides -

Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J; Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E; Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T; Pelet C, Schwope I, Ziebarth H;

26-MAR-2002; 2002WO-EP03401. 26-MAR-2001; 2001US-278333P.

WO200277272-A2.

03-OCT-2002.

Homo sapiens.

Synthetic.

(RPIG-) RPIGENOMICS AG.

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The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regularory regions in a subject. The method comprises contacting a target nucleic acid in a bological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid ABZD3861 to ABZ1118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cyrosine methylation state and/or single nucleotide polymorphisms (SNPB) of haematopoietic cell proliferation disorder related polymorphisms (SNPB) of haematopoietic cell proliferation disorder related missorder camplification of haematopoietic cell proliferation of sectoring a predisposition to, differentiation between also be used for detecting a predisposition to, differentiation between consumption can be used for detecting a predisposition to, differentiation between a highly specific classification of haematopoietic cell proliferative call proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders.
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1.1%; Score 13.8; DB 1; Length 18; 82.2%; Pred. No. 2.9e+02; ve 0; Mismatches 2; Indels
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                                                                                                                                                        AAQ47991 standard; DNA; 19
                                                                                                                             RESULT 210
AAQ47991
ID AAQ4799
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ABZ10595;

RESULT 209
ABZ10595
ID ABZ1059
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AC ABZ1059

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The Ligase Chain Reaction has been improved to increase the
"flexibility" or "dynamic range" of each probe set used in the
detection of small mutations (single base deletions, insertions and
changes, as well as multiple mutations where the size of the
mutation is less than about 15% of the average probe length).

Previously the determination of the genetic constituency of an
individual has been time consuming. The invention comprises reacting
probes and sample (suspected to contain the target nucleic acid)
under hybridising conditions that have been modified - 1. the
concentration of monovalent cation (Na+, K+, or NR3H+; R = H or
lower alkyl) is 100-200mM; 2. "hot start" (temp. range 50-95
ce degree C) may be used; and 3. one of the downstream probes has a
mismatch within 5 bases from the 5' end so it is not complementary
to the target sequence (The complementary probe is also mismatched).
These may be used either on their own or in conjunction.
AAG62245 and AAG62246 are used to detect the G551D mutation in
cystic fibrosis. The remaining probes are selected from AAG62247-50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ligase Chain Reaction - specific probe for CF mutation detection.
                                                                                                                                                                                                                                                        Improved ligase chain reaction with high monovalent cation conoras, mismatched probes and/or high initial mixing temps - used to detect small mutations in known DNA sequences, pref. for detecting cystic fibrosis mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cystic Fibrosis, CF missense mutation; improved method;
diagnosis; known mutation; Ligase chain reaction; G551D; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.1%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 3e+02; cive 0; Mismatches 2; Indels
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~hes 2; Indels
                                                                                                                                                         Gordon J, Hsieh W;
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                                                                                                                                                                                                                                                                                                                                                        Claim 24; Page 13; 64pp; English.
                                                                                                                                                         Fang P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1435 AATTICTIGCTGGTTGA 1451
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                                      93WO-US08359.
                                                                            92US-0951495.
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(first entry)
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Best Local Similarity 88.23
Matches 15; Conservative
                                                                                                                                                           Beaudet AL, Bouma SR,
                                                                                                                                                                                                                  WPI; 1994-135607/16.
                                                                                                                (ABBO ) ABBOTT
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                                      07-SEP-1993;
                                                                            25-SEP-1992;
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14-APR-1994.
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ID AAQ6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Two primer sets are used for detecting at least two mutations characteristic of cystic fibrosis, each set comprises two primer pairs: pair Pl comprises a primer specific for a normal allele and pair P2 comprises a primer specific for a mutant allele, each pair further comprises a common primer. PCR is performed on genomic DNA using both primer specific for a mutant allele indicates the likelihood that the parient carries a mutant allele indicates the likelihood fibrosis phenotype. This primer is designated G551D-N and is the primer see AAQ47990 and AAQ47992).

(Updated on 25-WAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosis of cystic fibrous - using allele specific multiplex polymerase chain reaction system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.1%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cystic Fibrosis; CF missense mutation; improved method; diagnosis; known mutation; Ligase chain reaction; G551D; ss.
                                                                                                                                        Cystic fibrosis; mutation; detection; primer; primer set; diagnosis; PCR; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                               PCR primer used in diagnosis of cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 4 A; 4 C; 4 G; 7 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 24; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1451
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                                                                                                                                                                                                                                                                                                                      93WO-US02259
                                                                                                                                                                                                                                                                                                                                                            92US-0850703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ62249 Standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (updated)
(first entry)
                                        (updated)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Fortina P, Surrey S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1993-303489/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                     409318177-A1
                                                                                                                                                                                                                                                                                                                      11-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                            13-MAR-1992;
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21-NOV-1994
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                                      25-MAR-2003
22-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                16-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                 Synthetic.
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  AA047991;
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Matches

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Gaps

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RESULT 214
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                                                                                                                                                                                                                                 The Ligase Chain Reaction has been improved to increase the "flexibility" or "dynamic range" of each probe set used in the detection of small mutations (single base deletions, insertions and changes, as well as multiple mutations where the size of the changes, as well as multiple mutations where the size of the mutation is less than about 15% of the average probe length). The previously the determination of the genetic constituency of an individual has been time consuming. The invention comprises reacting probes and sample (suspected to contain the target mucleic acid) individual has been time consuming. The invention occupies reacting probes and sample (suspected to contain the target mucleic acid) concentration of monovalent cation (Na+, K+, or NRJH+; R = H or lower alkyl) is 100-200mM; 2. "hot start" (temp. range 50-95 of edgree C) may be used; and 3. one of the downstream probes has a mismatch within 5 bases from the 5' end so it is not complementary to the target sequence (The complementary probe is also mismatched). These may be used either on their own or in conjunction.

These may be used either on their own or in conjunction.

Add62245 and AAQ62246 are used to detect the G551D mutation in cystic fibrosis. The remaining probes are selected from AAQ62247-50. This invention is also applicable to other disease related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                       concns., mismatched probes and/or high initial mixing temps -
used to detect small mutations in known DNA sequences, pref. for
detecting cystic fibrosis mutations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13.8; DB 1; Length 19;
Pred. No. 3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alfalfa Mosaic virus 4; influenza endonuclease, detection; electrophoresis; substrate cleavage; ss.
                                                                                                                                          improved ligase chain reaction with high monovalent cation
                                                                      Gordon J, Haieh W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/mod_base= Triphosphorylated-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19 BP; 4 A; 3 C; 4 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5' end fragment of Alfalfa Mosaic Virus 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= b
/mod_base= 2'-OMe-U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                               Claim 24; Page 13; 64pp; English.
                                                                     Fang P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1435 AATTICTIGCTGGTTGA 1451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT74905 standard; RNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.14;
               25-SEP-1992; 92US-0951495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 88.2
Matches 15; Conservative
                                                                     Bouma SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alfalfa Mosaic virus 4.
                                                                                                             WPI; 1994-135607/16
                                       (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified base
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                                                                     Beaudet AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutations.
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AAT74905
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This sequence represents the 5' end of Alfalfa Mosaic virus 4 RNA. This sequence was used in the method of the invention for detecting the enzyme activity in a sample. The method comprises: (a) adding an oligonucleotide substrate to a sample to generate an oligonucleotide product; (b) hybridising the oligonucleotide prod. with a DNA remplate which comprises a first segment complementary to the oligonucleotide and a 5' extension of at least one nucleotide attached to the 5' end of the DNA segment, such that a DNA:RNA hybrid or a DNA:DNA duplex is formed; (c) adding a DNA polymerase and labelled mononucleotides such the box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      that the DNA polymerase incorporates the monouncleotides to the 3 end of the oligomucleotide, and (d) measuring the amt. of labelled hybrid prod. as a measure of the amt. of the enzyme activity in the sample. The method is used to assay for enzymes e.g. endonuclease, exonuclease or ribozymes, that act on substrates to generate single stranded oligomucleotide prods. by cleaving the substrate which then forms a primer for extension by a DNA polymerase on a template. It can be used to identify the position where the enzyme cleaves the substrate. The assay can also be used to screen for inhibitors of these enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                   Detection of enzyme pref. endonuclease or ribozyme, in a sample by cleavage of an RNA substrate to generate a primer for a labelled
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%; Score 13.8; DB 1; Length 19
17.6%; Pred. No. 3e+02;
ative 12; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5' end fragment of Alfalfa Mosaic Virus 4.
                                                                                                                                                                                                                                                                                                                                                                                                             Examples; Page 14; 34pp; English
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                                                                                                                                                                                                                                                                                                                                                               polymerase extension reaction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT49298 standard; RNA; 19 BP.
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                                                 96WO-US08330
                                                                                                  95US-0487760
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Best Local Similarity 17.00.
These 3; Conservative
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                                                                                                                                                   & CO INC
                                                                                                                                                                                                                                                     WPI; 1997-052365/05.
                                                                                                                                                                                                    Cole JL, Kuo LC,
                                                                                                                                                   MERI ) MERCK
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                                              03-JUN-1996;
                                                                                               07-JUN-1995;
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19-DEC-1996
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Olsen DB;

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AMA 7264-T47280 represent capped RNA molecules produced by the method of the invention is for producing capped RNA con congrises reacting a RNA or analogue. The method comprises reacting a RNA or analogue coligonucleotide with a phosphate addition agent to form a RNA or analogue mono-, di- or triphosphate, which is then capped. The presence of the cap is important for mRNA maturation, initiation of translation, and protects the mRNA against various RNases present in the cell. The capped RNA or analogue is an influenza endonuclease aptamer, useful for capped RNA or analogue is an influenza infection in an animal. The synthetic capped RNA are substrates for virally encoded endonuclease associated with influenza virus. The short non-extendible (due to their length or because of the modification of the 3' end of the oligo) RNA molecules are potent inhibitors of the clavage of capped RNA by influenza condonuclease. They may be used to investigate viral and cellular mechanisms of transcription/translation, or mRNA maturation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Capped RNA molecule, mRNA maturation, translation initiation, influenza, endonuclease aptamer; RNase; therapy; inhibitor; 88.
                                                                                                                                                                                                                  Production of capped RNA or analogues - useful as substrates for
influenza virus associated virally encoded endonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.1%; Score 13.8; DB 1; Length 19; Best Local Similarity 17.6%; Pred. No. 30+02; Matches 3; Conservative 12; Mismatches 2; Indels
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/mod_base= 2'-deoxy-2'-fluoro-adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Capped RNA influenza endonuclease substrate #4.
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/mod_base= 2'-0-methyluridine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;
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/mod_base= triphosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches
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                                                                                                                                                                                                                                                                                                Claim 18; Page 13; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1521 TETATETETETAGITE 1537
                                                                                                                        Kuo LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 UUUUUAUUUUUAAUUUU 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT47270 standard; RNA; 19 BP
                     95US-0480068.
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                                                                        (MERI ) MERCK & CO INC.
                                                                                                                        Cole JL,
                                                                                                                                                                     WPI; 1997-051868/05
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                     07-JUN-1995;
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                                                                                                                        Benseler F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT47270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                             This sequence represents the 5' end of Alfalfa Mosaic virus 4 RWA.

This sequence was used as a substrate for influenza endomuclease in the method of the invention. The method allows detection of influenza endomuclease activity in a sample and comprises: (a) adding an influenza endomuclease substrate to a sample and comprises: (a) adding an influenza endomuclease substrate to a sample to generate an RNA product; (b) hybridising the RNA prod. with a DNA template which comprises a first segment complementary to the RNA and a 5' extension of at least one nucleotide attached to the FNA and a 5' extension of at least one nucleotide attached to the 5' end of the DNA segment, such that a DNA:RNA hybrid is formed; (c) adding a DNA polymerase and labelled monourlectides such that the DNA polymerase incorporates the monourlectides to the 3' end of the RNA in the RNA:DNA duplex; and (d) measuring the amount of labelled hybrid prod. as a measure of the monour of influenza endomuclease activity. The method is used to quantitate which then forms a primer for extension by a DNA polymerase on a template. The assay does not influenza endomuclease by cleaving the RNA substrate which then forms a primer for extension by a DNA polymerase the amount of influenza endomuclease by cleaving the RNA substrate which then forms a primer for extension by a DNA polymerase the amount of substrate the amount of influenza endomuclease by cleaving the SNA substrate which then forms a primer for extension by a DNA polymerase the thus may be run in a 96-well microtitre plate. The assay also monitors substrate cleavage at the correct position thereby discriminating against non-specific cleavage products.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Capped RNA molecule; mRNA maturation; translation initiation; influenza; endonuclease aptamer; RNaBe; therapy; inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                          Detection of influenza virus endonuclease in a sample - by cleavage of an RNA substrate to generate a primer for a labelled polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.1%; Score 13.8; DB 1; Length 19; Best Local Similarity 17.6%; Pred. No. 3e+02; Matches 3; Conservative 12; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Capped RNA influenza endonuclease substrate #3.
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/mod_base= 2'-deoxyadenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mod_base= triphosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                          Claim 6; Page 12; 28pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                    AAT47264-T47280 represent capped RNA molecules produced by the method of the invention. The method of the invention is for producing capped RNA or RNA analogues. The method comprises reacting a RNA or analogue oligonucleotide with a phosphate addition agent to form a RNA or analogue mono., di- or triphosphate, which is then capped. The presence of the cap is important for mRNA maturation, initiation of translation, and protects the mRNA against various RNases present in the cell. The capped RNA or analogue is an influenza endonuclease aptamer, useful for treating or preventing an influenza endonuclease aptamer, useful for capped RNA are substrates for virally encoded endonuclease associated with influenza virus. The short non-extendible (due to their length or because of the modification of the 3' end of the oligo) RNA molecules are content inhibitors of the cleavage of capped RNA by influenza endonuclease. They may be used to investigate viral and cellular endonuclease. They may be used to investigate viral and cellular
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influenza virus associated virally encoded endonuclease
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/mod_base= 2'-deoxy-2'-fluoro-uridine
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/mod_base= 2'-deoxy-2'-fluoro-uridine
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17.6%; Pred. No. 3e+02;
tive 12; Mismatches
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/mod_base= triphosphorylated
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                                                                                                                                  Benseler F,
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AAT47264-T47280 represent capped RNA molecules produced by the method of the invention is for producing capped RNA or nalogues. The method comprises reacting a RNA or analogue.

Or RNA analogues. The method comprises reacting a RNA or analogue.

Cligomuclectide with a phosphate addition agent to form a RNA or analogue mono., di- or triphosphate, which is then capped. The presence of the cap is important for mRNA maturation, initiation of translation, and protects the mRNA against various RNAses present in the cell. The capped RNA or analogue is an influenza endonuclease aptamer, useful for treating or preventing an influenza endonuclease aptamer, useful for capped RNA are substrates for virally encoded endonuclease associated with influenza virus. The short non-extendible (due to their length or because of the modification of the 3' end of the oligo) RNA molecules are content inhibitors of the cleavage of capped RNA by influenza concurred the short mouse of the oligo) RNA molecules are endonuclease. They may be used to investigate viral and cellular mechanisms of transcription/translation, or mRNA maturation.
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tive 12; Mismatches 2; Indels
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Olsen DB;

& CO INC

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ART47264-T47280 represent capped RNA molecules produced by the method of the invention is for producing capped RNA correction. The method of the invention is for producing capped RNA analogues. The method comprises reacting a RNA or analogue.

Or RNA analogues. The method comprises reacting a RNA or analogue collisions analogue mono, di- or triphosphate, which is then capped. The presence of the cap is important for mRNA maturation, initiation of translation, and protects the mRNA against Various RNases present in the cell. The capped RNA or analogue is an influenza endonuclease aptemer, useful for treating or preventing an influenza infection in an animal. The synthetic capped RNA are substrates for virally encoded endonuclease associated with influenza virus. The short non-extendible (due to their length or pecause of the modification of the 3' end of the oligo) RNA molecules are potent inhibitors of the cleavage of capped RNA by influenza may be used to investigate viral and cellular mechanisms of transcription/translation or mechanisms of transcription or mechanisms.
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the invention. The method of the invention is for producing capped RNA the invention. The method of the invention is for producing capped RNA or RNA analogues. The method comprises reacting a RNA or analogue coligonucleotide with a phosphate addition agent to form a RNA or analogue mono, di- or triphosphate, which is then capped. The presence of the cap is important for mRNA maturation, initiation of translation, and protects the mRNA against various RNases present in the cell. The capped RNA or analogue is an influenza endonuclease aptamer, useful for capped RNA are substrates for varially encoded endonuclease associated with influenza virus. The short non-extendible (due to their length or capped RNA are substrates for virally encoded endonuclease associated with influenza virus. The short non-extendible (due to their length or because of the modification of the 3' end of the oligo) RNA molecules are potent inhibitors of the cleavage of capped RNA by influenza endonuclease. They may be used to investigate viral and cellular endonuclease. They may be used to investigate viral and cellular
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/mod_base= 2'-0-methyluridine
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'mod_base= triphosphorylated
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                                                                                                                                                            Kuo LC,
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Matches
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Gaps

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/*tag= c /note= "biotin labelled for attachment to solid support"

/*tag= b /mod_base= 2'-0-methyluridine 'mod base= triphosphorylated

Location/Qualifiers

*tag=

(first entry)

schultz143-3.rng

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ANT47264-T47280 represent capped RNA molecules produced by the method of the invention is for producing capped RNA correct analogues. The method comprises reacting a RNA or analogue correct analogue method comprises reacting a RNA or analogue coligonucleotide with a phosphate addition agent to form a RNA or analogue mono-, di- or triphosphate, which is then capped. The presence of the cap is important for mRNA maturation, initiation of translation, and protects the mRNA against various RNases present in the cell. The capped RNA or analogue is an influenza endonuclease aptamer, useful for capped RNA are substrates for virally encoded endonuclease associated with influenza virus. The short non-extendible (due to their length or because of the modification of the 3' end of the oligo) RNA molecules are potent inhibitors of the cleavage of capped RNA by influenza condonuclease. They may be used to investigate viral and cellular mechanisms of transcription/translation, or mRNA maturation.
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                                                                                                                           Production of capped RWA or analogues - useful as substrates for influenza virus associated virally encoded endonuclease
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17.6%; Pred. No. 3e+02;
tive 12; Mismatches 2; Indels
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/mod_base= triphosphorylated
                                            Olsen DB;
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                                            Kuo LC,
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(MERI ) MERCK & CO INC.
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                                          Benseler F, Cole JL,
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Matches 3; Conserv
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Or RNA analogues. The method comprises reacting a RNA or analogue cor in the method comprises reacting a RNA or analogue and in important for mRNA maturation, initiation of translation, of the cap is important for mRNA maturation, initiation of translation, and protects the mRNA against various RNAses present in the cell. The capped RNA or analogue is an influenza endonuclease aptamer, useful for treating or preventing an influenza infection in an animal. The synthetic capped RNA are substrates for virally encoded endonuclease associated with influenza virus. The short non-extendible (due to their length or because of the modification of the 3' end of the oligo) RNA molecules are potent inhibitors of the cleavage of capped RNA by influenza endonuclease. They may be used to investigate viral and cellular endantsms of transcription/translation, or mRNA maturation.
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17.6%; Pred. No. 3e+02;
7ative 12; Mismatches 2; Indel8
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/mod_base= triphosphorylated
                                                                                                                                Olsen DB;
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96WO-US08394
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Best Local Similarity 17.6
Matches 3; Conservative
                                                                                    (MERI ) MERCK & CO INC
                                                                                                                                Cole JL,
                                                                                                                                                                        WPI; 1997-051868/05.
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Synthetic

AAT47264;

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the invention. The method of the invention is for producing capped RNA consists analogues. The method comprises reacting a RNA or analogue RNA consists analogues. The method comprises reacting a RNA or analogue coligonucleotide with a phosphate addition agent to form a RNA or analogue mono, di- or triphosphate, which is then capped. The presence of the cap is important for mRNA maturation, initiation of translation, and protects the mRNA against various RNAsses present in the cell. The capped RNA or analogue is an influenza endonuclease aptamer, useful for capped RNA are substrates for virally encoded endonuclease associated with influenza virus. The short non-extendible (due to their length or because of the modification of the 3' end of the oligo) RNA molecules are potent inhibitors of the cleavage of capped RNA by influenza continuates in the cleavage of capped RNA by influenza continuation. The charage of capped RNA by influenza continuations of the cleavage of capped RNA by influenza continuation translation, or mRNA maturation.
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influenza virus associated virally encoded endonuclease
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/mod base= 2'-O-methyluridine
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'cod base= triphosphorylated
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AAT47264-T47280 represent capped RNA molecules produced by the method of the invention is for producing capped RNA control or RNA analogues. The method comprises reacting a RNA or analogue cor RNA analogues. The method comprises reacting a RNA or analogue coligonucleotide with a phosphate addition agent to form a RNA or analogue mono. di- or triphosphate, which is then capped. The presence of the cap is important for mRNA maturation, initiation of translation, and protects the DRNA against various RNases present in the cell. The capped RNA or analogue is an influenza endomuclease aptamer, useful for treating or preventing an influenza endomuclease aptamer, useful for capped RNA are substrates for virally encoded endonuclease associated with influenza virus. The short non-extendible (due to their length or because of the modification of the 3' end of the oligo) RNA molecules are often inhibitors of the cleavage of capped RNA by influenza potent inhibitors of the cleavage of capped RNA by influenza endomuclease. They may be used to investigate viral and cellular endomuclease. They may be used to investigate viral and cellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Capped RNA molecule; mRNA maturation; translation initiation; influenza; endonuclease aptamer; RNase; therapy; inhibitor; ss.
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                                                                                                                                                                                                                                                                                                                              1.1%; Score 13.8; DB 1; Length 19;
17.6%; Pred. No. 3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Capped RNA influenza endonuclease substrate #10.
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/mod_base= 2'-0-methyluridine
                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;
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'mod_base= triphosphorylated
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/mod_base= phosphorothioated
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            Claim 18; Page 15; 39pp; English
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WPI; 1997-051868/05.
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                     AAT47264-T47280 represent capped RNA molecules produced by the method of the invention is for producing capped RNA caralogues. The method comprises reacting a RNA or analogue CARA analogues. The method comprises reacting a RNA or analogue CARA analogues. The method comprises reacting a RNA or analogue CARA analogue mono-, di- or triphosphate, which is then capped. The presence of the cap is important for mRNA maturation, initiation of translation, or translation, and protects the mRNA against various RNases present in the cell. The capped RNA or analogue is an influenza endonuclease aptamer, useful for treating or preventing an influenza infection in an animal. The synthetic capped RNA are substrates for virally encoded endonuclease associated with influenza virus. The short non-extendible (due to their length or because of the modification of the 3' end of the oligo) RNA molecules are coptent inhibitors of the clavage of capped RNA by influenza condonuclease. They may be used to investigate viral and cellular endonuclease. They may be used to investigate viral and cellular methods are condonuclease. They may be used to investigate viral and cellular captangents.
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17.6%; Pred. No. 3e+02;
trive 12; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Capped RNA influenza endonuclease substrate #11.
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/mod_base= triphosphorylated
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/mod_base= phosphorothioated
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Claim 18; Page 15; 39pp; English
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Beet Local Similarity 17.00.
3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                             RESULT 225
AAT47279
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AAT47264-T47280 represent capped RNA molecules produced by the method of the invention is for producing capped RNA or Rablogues. The method comprises reacting a RNA or analogue and or the method comprises reacting a RNA or analogue. The method comprises reacting a RNA or analogue coligonucleotide with a phosphate addition agent to form a RNA or analogue mono-, di- or triphosphate, which is then capped. The presence of the cap is important for mRNA maturation, initiation of translation, and protects the mRNA against various RNases present in the cell. The capped RNA or analogue is an influenza enfoncelease aptemer, useful for treating or preventing an influenza infection in an animal. The synthetic capped RNA are substrates for virally encoded endonuclease associated with influenza virus. The short non-extendible (due to their length or because of the modification of the 3' end of the oligo) RNA molecules are potent inhibitors of the cleavage of capped RNA by influenza endonuclease. They may be used to investigate viral and cellular endonuclease. They may be used to investigate viral and cellular endonuclease of transcription/translation, or mRNA maturation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rb gene; antisense oligonucleotide; modulate; gene expression; ss.
substrates for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1%; Score 13.8; DB 1; Length 19; 17.6%; Pred. No. 3e+02; tive 12; Mismatches 2; Indels
Production of capped RNA or analogues - useful as substi
influenza virus associated virally encoded endonuclease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rb gene antisense oligonucleotide rb-N-71.
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Matches 3; Conservative
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schultz143-3.rng

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cc effective downregulation of negative growth control by rb, while oligonuclectides AN49052-236 had little effect. The oligonuclectides conjugurations the specification describes oligonuclectides conformation. The specification describes oligonuclectides that contrain 8-30 nuclectides, which contain at most 8 nuclectides and conscious consecutive nuclectides able to form three H-bonds each to four consecutive ordesines; do not contain two sequences of three consecutive consecutive consecutive consecutive consecutive consecutive consecutive consecutive consecutive bonds (3R) is given by 2R/3R = 0.33-0.72. The nucleotides acts able to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The consecutive conformation of primary cell cultures (e.g. bone marrow seem, liver or proliferation of primary cell cultures (e.g. bone marrow seem, liver or kidney cells, osteoblasts and/or keratinocytes). The coligonuclectides can also be used to analyse function of proteins (by altering their expression or activity) and therapeutically, e.g. in cases of cancer or (targeting TGF) for stimulating the immune system.
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Sequence 19 BP; 6 A; 1 C; 1 G; 11 T; 0 other;

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1.1%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 3e+02; tive 0; Mismatches 2; Indels
                                                                                       1172 TTTATTAGATAAATTTC 1188
                          Best_Local Similarity 88,2
Matches 15, Conservative
      Query Match
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Gaps

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AAV26328 standard; DNA; 19
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RESULT 227
                                      AAV26328

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 AAV2
 AAV3
 AAV2
 AAV2
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BB

Human prostate cancer marker UC Band #201 identifying RT-PCR primer 1.

(first entry)

Prostate cancer; human; marker; diagnosis; treatment; RT-PCR primer; ss.

Homo sapiens. Synthetic

WO9804689-A1

05-FEB-1998.

96WO-US12516. 31-JUL-1996; 96WO-US12516 31-JUL-1996;

(UROC-) UROCOR INC.

Veltri R; Ralph D, O'hara SM, An G,

Novel biallelic markers used to construct a high density disequilibrium

Chumakov

Cohen D, Blumenfeld M,

WPI; 2000-013267/01.

Claim 8; Page 2110; 2745pp; English.

map of the human genome

AA265654 to AA269578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nuclectie sequences. AA269579 to AA27740 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haploryping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and disgnostic methods, as well as the characterisation of the differential efficacious responses to and side

effects from pharmaceutical agents acting on a disease as well as other

rreatment. N.B. The SEQ 1D NOB 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297

WPI; 1998-130681/12.

Human prostate cancer marker - useful for detection and treatment of human prostate cancer

Example 4; Page 120; 229pp; English.

This primer is used in the relative quantitative RT-PCR to examine the expression of the genes which is used for the identification of markers of human prostate cancer. Isolated nucleic acid segments shown in AAV16881 to AAV16882, AAV16890 to AAV16903, AAV26351 and AAV26352 which can act as human prostate cancer markers are provided in the specification. The specification also provides methods for identifying markers for human prostate cancer and for detection of prostate cancer earls. The markers can be identified by amplifying human prostate RNA to provide nucleic acid amplification products, separating the products and identifying those RNA that are differentially expressed between human

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prostate cancers versus normal or benign human prostate. Prostate cancer cells in a sample can be detected by detecting a nucleic acid in a sample, the nucleic acid being a prostate cancer marker. Primers and probes derived from this marker can be used for the detection of prostate cancer cells in a sample. Antibodies against the protein encoded by the marker nucleic acid fragments, inhibitors of the protein and oligomucleotides autisense to the markers can be used in the treatment of prostate cancer. The antibodies can also be used for the diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                 Human biallelic marker downstream amplification primer SEQ ID NO:8817.
                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome, biallelic marker, high density disequilibrium map, genomic map, haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer; amplification; single nucleotide polymorphism; SNP; PCR primer;
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                                                                                                                                                                      Query Match
1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                          Sequence 19 BP; 9 A; 2 C; 4 G; 4 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                 AAZ74461 standard; DNA; 19 BP
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                                                                                                                  human prostate cancer.
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                                                                                                                                                                                                                                                                                                    RESULT 228
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The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme [1] which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (MNP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule [11] comprising a promoter operably linked to a nucleic acid segment encoding [1]. [1] can have antipsoriatic, ophthalmological, cytostatic, antiseborrheic, antidiabetic, antisickling, cphthalmological, cytokine involved in inflammation. [1] can be used in gene therapy. [1] and [11] are useful for treating proliferative skin diseases such as psoriadis, atopic dermatitis, actinic keratosis, skin diseases such as psoriadis, atopic dermatitis, actinic keratosis, squamous or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diseases. Computating retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing scarring such as keloid, adhesion and hypertrophic or hypertrophic burn and an analyse of the scarring such as keloid, adhesion and hypertrophic or hypertrophic burn and an analyse of the scarring such as keloid, adhesion and hypertrophic or hypertrophic burn and an analyse of the scarring such as keloid, adhesion and bypertrophic or hypertrophic burn and some 
                                                                                                                                                                                  Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnerary; proliferative disease; skin disease; psoriasis; diabetic retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP; matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide; antisickling; ophthalmological; keratolytic; gene therapy; viral wart; basal cell carmaticis; actinic keratosis; squamous cell carcinoma; scorrein eickle cell retinopathy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent
                                                                                                                               Cdk-we-hu ribozyme binding site SEQ ID NO:1267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 164; 408pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-OCT-2000; 2000WO-US29500
                                                                 10-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robbins JM, Tritz R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMMU-) IMMUSOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-300427/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200130362-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-MAY-2001.
      AAH58843;
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Representative examples of ribozyme recognition sites are given in AAAS2415 to AAA86787. The ribozyme of the invention is useful for inhibiting restences by introduction of the ribozyme is resistant to and anomuclease activity and hence is efficient in restences treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1 -
                                                                                                                                                                                                                                  Gaps
and 3367, are not actually given a sequence in the Sequence Listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a hairpin or hammerhead ribozyme,
                                                                                                                                                                                                                               ö
                                                                                                                                                              DB 1; Length 19;
                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
                                                                                                                                                       1.1%; Score 13.8; DB 1
BB.2%; Pred. No. 3e+02;
Live 0; Mismatches
                                                                                            Sequence 19 BP; 11 A; 6 C; 1 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 7 A; 4 C; 3 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robbins JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cdk-we-hu ribozyme binding site #156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 65; 109pp; English.
                                                                                                                                                                                                                                                                                         1208 AACAAACAAACAATTGG 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Welch PJ, Barber JR,
                                                                                                                                                                                                                                                                                                                                                    1 AACAACAACAACTAG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0110954.
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                                  from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA83681 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-2000 (first entry)
                                                                                                                                                                                      Local Similarity 88.2
les 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-412314/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restenosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA83681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marmalia
                                                                                                                                                                 Query Match
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Matches
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99US-0161532.

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                           1.1%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 3e+02; ative 0; Mismatches 2; Indels
Seguence 19 BP; 7 A; 4 C; 3 G; 5 T; 0 other;
                                                                                              1378 TACGGAATAATGAGTTA 1394
                                                                                                                             2 TACAGAATCATGAGTTA 18
                                                                Conservative
                                             Local Similarity
les 15; Conserv
                                Query Match
                                                              Matches
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Gaps

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1.1%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 3e+02; tive 0; Mismatches 2; Indels

Query Match
Best Local Similarity 88.2
Matches 15, Conservative

1378 TACGGAATAATGAGTTA 1394

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racadaarcardagrin 18

AAH58843 standard; DNA; 19 BP

230

RESULT 23
AAHS8843
ID AAHS

RESULT 231

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17; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection;
                                                Human leukocyte gene expression profiling probe SEQ ID NO 1784.
      ABZ01793 standard; DNA; 50 BP.
                                                                                                                                          22-OCT-2001; 2001WO-US47856.
                                                                                                                                                         20-OCT-2000; 2000US-241994P.
08-JUN-2001; 2001US-296764P.
                                  (first entry)
                                                                                                               WO200257414-A2
                                                                                                  Homo sapiens.
                                  09-JAN-2003
                                                                                                                             25-JUL-2002.
                                                                                    probe; ss.
ABZ01793/c
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Altman P, Prentice J, Phillips J; Johnson F; Quertermous T, Matcuk G, wohlgemuth J, Fry K, Ly N, Woodward R, Qu (BIOC-) BIOCARDIA INC.

WPI; 2002-636525/68.

monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides New system for leukocyte expression profiling, diagnosing a disease, monitoring (the rate of) progression of a disease, e.g. atherosclero

Claim 1; Page 382; 2038pp; English.

The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ008152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection.

Sequence 50 BP; 17 A; 8 C; 13 G; 12 T; 0 other;

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Gaps
                        ö
 Length 50;
                        17; Indels
 Score 13.8; DB 1;
Pred. No. 4.7e+02;
                        0; Mismatches
            58.58;
                        24; Conservative
Query Match
Best Local Similarity
                         Matches
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AAD26678 standard; DNA; 15 BP

Human GPR31 gene polymorphism detecting ASO primer #1. (first entry) 26-MAR-2002

Human; G-protein coupled receptor 31; GPR31 protein; haplotyping;

The invention relates to genetic variants of human G-protein coupled receptor 31 (GPR31) gene. The invention also relates to compositions and methods for haplotyping and/or genotyping the GPR31 gene in an individual. Polymuclectides of the invention are useful in studying the expression and function of GPR31, and in expressing GPR31 protein for use in screening candidate drugs to treat diseases related to GPR31 activity and in studying the effect of the variation on the biological activity of GPR31 as well as on the binding affinity of candidate drugs targetting GPR31 for the treatment of cancer. They are also used in gene therapy. The haplotyping method is useful for improving the efficiency and reliability of several steps in the discovery and development of drugs for treating diseases associated with GPR31 activity. e.g. cancer. This method is also useful for haplotyping GPR31 activity e.g. cancer. This method is also useful for the pharmaceutical research scientist to validate GPR31 as a candidate carget for, and in design of clinical trials of candidate drugs, for treating a specific condition drugs or disease predicted to be associated with GPR31 activity. The present sequence is an allele specific objective objective objective objective (ASO) primer used to detect human GPR31 Novel genetic variants of G-protein coupled receptor gene useful imstudying expression and function of the protein, and for screening drugs to treat diseases e.g. cancer genotyping; gene therapy; cancer; polymorphism; ASO; primer; allele-specific oligonucleotide; ss. Messer C; Lee 瑶, Kazemi A, Claim 16; Page 13; 75pp; English. (GENA-) GENAISSANCE PHARM INC 23-MAY-2001; 2001WO-US16908. 23-MAY-2000; 2000US-206572P. Bieglecki KM, Duda A, WPI; 2002-089915/12. gene polymorphisms WO200190124-A2 Homo gapiens 29-NOV-2001

Gaps ö 1.1%; Score 13.6; DB 1; Length 15; 12.9%; Pred. No. 2.7e+02; ve 1; Mismatches 0; Indels Sequence 15 BP; 10 A; 0 C; 1 G; 3 T; 1 other; Local Similarity 92.9%; nes 13; Conservative Query Match Best Loc Matches

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RESULT 233

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Nucleotide sequence of a PCR primer #1. ABQ79871 standard; DNA; 20 BP. (first entry) 23-DEC-2002 ABQ79871; ABQ7987. 8X8X8X8X8X8X8X8

Polymerase chain reaction; thermal cycle; immobilisation; genetic engineering; PCR; primer; ss.

Synthetic.

JP2002191369-A.

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The invention relates to a novel method for synthesising a target base sequence-containing nucleic acids. The method comprises the formation of single-stranded nucleic acids; synthesis of complementary strand by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthesizing target base sequence-containing nucleic acids constituting complementary base sequences against template by the LAMP method, applicable in identifying genetic diseases, cancerization and microrganisms -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthesising, target base sequence, annealing, genetic disease, SNP, single nucleotide polymorphism, cancer; PCR; primer; ss.
                                                                                                                                                                  This sequence is an example of a 2-5A-antisense oligonucleotide chimeric molecule. The antisense region targets the chimeric molecule to a particular region of RNA to be specifically cleaved and the 2',5'-linked tetraadenylate tail activates the 2-5A RNAse. Typical applications are treatment of viral infections (esp. for cleaved of a RNA virus genome), cancer; leukaemia, cardiovaecular disorders (e.g. restenosis after angioplasty), genetic disorders, osteoarthritis or rheumatoid
                                                                      Specific cleavage of RNA, useful partic. for treating viral infection, cancers, etc. - by using anti-sense oligo:nucleotide coupled to activator of 2-5A dependent RNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid synthesising method related PCR primer, SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                              1.1%; Score 13.6; DB 1; Length 22; 80.0%; Pred. No. 3.8e+02;
               Torrence
                                                                                                                                                                                                                                                                                                               (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                              Sequence 22 BP; 4 A; 0 C; 0 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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             Silverman R,
                                                                                                                                                                                                                                                                                                                                                                                                                                            1560 AAATTTTTTTTTTTTTTTT 1579
                                                                                                                                        Example 1; Page 68; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AAArritariririririr 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AALS5126 standard; DNA; 30 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-2001; 2001JP-0137060.
18-JUN-2001; 2001JP-0184131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-2002; 2002WO-JP04479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIKE ) EIKEN KAGAKU KK
             Maitra R,
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                             WPI; 1994-151315/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
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             Lesiak K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL55126;
                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                          The invention relates to performing a thermal cycle of PCR by using a substrate on which a deoxyribonucleic acid (DNA) is immobilized. The method is useful in the medical, biochemical, molecular biological and genetic engineering fields. Sequences ABQ79871-881 represent PCR primers used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2',5'-linked tetraadenylate-antisense oligonucleotide chimeric mol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a 2,,5'-linked tetraadenylate
"nucleotides linked through phosphodiester
bonds at hydroxyl groups of 2' and 5'
                                                                                                                                                                                 Carrying out a thermal cycle of polymerase chain reaction (PCR) lusing a substrate on which a DNA is immobilized used in medical, biochemical, molecular biological and gene engineering fields -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator; RNA cleavage; antiviral therapy; chimeric molecule; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.6; DB 1; Length 20;
Pred. No. 3.5e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 other;
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/*tag= b
/note= "antisense region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLEVELAND CLINIC RES INST.
US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ64706 standard; cDNA to mRNA; 22 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Examples; Page 9; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AAATHTTTTTTTTTTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                            1.1%;
                                        27-DEC-2000; 2000JP-0399573.
                                                                        27-DEC-2000; 2000JP-0399573.
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(first entry)
                                                                                                     (TOJO ) TOYO KOHAN CO LTD.
(TAKA/) TAKAHASHI K.
                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                    WPI; 2002-630904/68.
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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17-SEP-1993;
           09-JUL-2002
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04-JAN-1995
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Gaps

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RESULT 237
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annealing; and producing single-etranded nucleic acid from a target base sequence by the synthesis of a complementary strand by annealing of a complementary base sequence. The method is useful for synthesising a target base sequence-containing nucleic acids, which is applicable in detecting SNP (single nucleotide polymorphism) in genes, identifying genetic diseases, cancer and microorganisms. Such a method can be easily, rapidly and freely carried out without being influenced by contamination or complicated temperature control, but with improved reaction specificity, high accuracy and efficiency, operable at low cost. This polynucleotide sequence represents a PCR primer used in the synthesising method of the invention.
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                Mouse TNF-a hammerhead ribozyme target sequence (nt position 1326).
                                                                                                                                                                                                                                                                                                                                                                                     Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; TRTanslocation; chronic myel-jogenous leukeamia; CML; cancer; philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction, stroke; restenosis; transplant rejection; theumatoid arthritis; psoriatis; myocardial; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
                                                                                                                                                                                  ő
                                                                                                                                                         / Match 1.1%; Score 13.6; DB 1; Length 30; Local Similarity 67.9%; Pred. No. 4.6e+02; nes 19; Conservative 0; Mismatches 9; Indels
                                                                                                                                                             . 4.6e+02;
. 4.6e+02;
. . . 9; Indels
                                                                                                                                     Sequence 30 BP; 15 A; 2 C; 2 G; 11 T; 0 other;
                                                                                                                                                                                                       753 ATGTGATATTTGAAGCATCACATAAAA 780
                                                                                                                                                                                                                             3 ATTIGATGCTTAAATAATACATAATA 30
                                                                                                                                                                                                                                                                                     AATS6350 standard; RNA; 15 BP
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94US-0311486.
94US-0311749.
94US-0314397.
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94US-0227958.
94US-0228041.
94US-0245736.
94US-0271280.
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94US-0292620.
94US-0293520.
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94US-0218934.
94US-0222795.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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14-MAY-1997
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28-SEP-1994;
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06-JUL-1994
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                                                                                                                                                            Query Match
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                                                                                                                                                                                   Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNR-alpha mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed any synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit TNR-alpha expression, making them potentially useful for treating rheumatoid arthritis, septic shock and other inflammatory disorders including psoriasis, as well as
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Best Local Similarity 26.7%; Pred. No. 2.9e+02;
Matches 4; Conservative 10; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cor treatment of AIDS.
(Updated on 25-MAR-2003 to correct PI field.)
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94US-0319492.
94US-0321993.
94US-0334847.
94US-0337608.
94US-0345516.
94US-0357577.
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1 AUUAUUAUUAUUAUUU 15
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(first entry)
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                                 11-OCT-1994;
04-NOV-1994;
10-NOV-1994;
28-NOV-1994;
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14-MAY-1997
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RESULT 238

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Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
                                   9508 - 0380734,
9405 - 020109,
9405 - 02018934,
9405 - 0202483,
9405 - 0227958,
9405 - 0227958,
9405 - 0245736,
9405 - 0245736,
9405 - 0291932,
9405 - 0291932,
9405 - 0291932,
9405 - 0291932,
9405 - 0291932,
9405 - 0291433,
9405 - 0291433,
9405 - 0311486,
9405 - 0311486,
9405 - 0311486,
9405 - 0314847,
9405 - 0314847,
9405 - 0334847,
9405 - 0334847,
9405 - 0337608,
                         95WO-IB00156
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WO9523225-A2
                        23-FEB-1995;
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06-JUL-1994;
15-AUG-1994;
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17-AUG-1994;
19-AUG-1994;
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            31-AUG-1995
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04-APR-1994
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Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Stinm S, Karpeisky A, Kisich K, Matulic-adamic J, McBwiggen JA; Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D; Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T; (RIBO-) RIBOZYME PHARM INC.

Ribozymes having modified bases and methods for producing them for use in inhibiting disease related genes

Claim 2; Page 252; 407pp; English.

The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves TWR-alpha mRNA at the nucleotide base position indicated in the DE line. Segions of the mRNA that do not form secondary folding structures and that contain potential harmerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed any synthesised with modifications that improve their nuclease sequences and thereby inhibit TWF-alpha expression, making them potentially useful for treating rheumatoid architis, septic shock and other inflammatory disorders including psoriasis, as well as for treatment of AIDS.

(Updated on 25-MAR-2003 to correct PI field.)

0; Gaps Query Match
1.1%; Score 13.4; DB 1; Length 15;
Best Local Similarity 26.7%; Pred. No. 2.9e+02;
Matches 4; Conservative 10; Mismatches 1; Indels

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1039 ATTTATTATTATGT 1053 |:::|::|::| AUUUAUUAUUUAUUU 15

Š 셤 The present sequence represents a preferred target sequence for an

Claim 2; Page 252; 407pp; English.

Mouse TNF-a hammerhead ribozyme target sequence (nt position 1313). Stinchcomb DT, Chownira B, Direnzo A, Draper KG, Dudycz LW; Stinm S, Karpelsky A, Kisich K, Matulic-adamic J, Mcswiggen JA; Modak A, Pavco P, Beigleman L, Sullivan SW, Sweedler D; Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T; Enzymatic nucleic acid, ribozyme, trans cleavage, inhibition, penzymession; downregulation; interleukin-5; ll-5; lC3M-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psortasis; myocardial isobaemia; Kasasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; Ribozymes having modified bases and methods for producing them for use in inhibiting disease related genes AAT56332 standard; RNA, 15 BP. 940S-0303039. 940S-0311486 940S-0311499. 940S-0316771. 940S-0316771. 940S-0321993. 940S-0334847. 940S-0337608. 940S-035516. 940S-035533. 95US-0380734. 94US-0201109. 94US-0218934. 94US-022795. 94US-0224483. 94US-0228041. 94US-0245736. 94US-0271280. 94US-0291932. 94US-0291433. 94US-0292620. 94US-0293520. 94US-0300000. 95WO-IB00156 (RIBO-) RIBOZYME PHARM INC. (updated)
(first entry) WPI; 1995-35109D/45. 16-AUG-1994; 17-AUG-1994; 19-AUG-1994; 02-SEP-1994; 08-SEP-1994; 23-SEP-1994; 23-SEP-1994; Mus musculus. 07-APR-1994; 15-APR-1994; 15-APR-1994; 18-MAY-1994; 06-JUL-1994; 15-AUG-1994; 28-SEP-1994; 03-OCT-1994; 07-OCT-1994; 11-0CT-1994; 04-NOV-1994; 10-NOV-1994; 28-NOV-1994; WO9523225-A2 23-FEB-1995; 16-DEC-1994; 25-MAR-2003 14-MAY-1997 31-AUG-1995 23-FEB-1994 29-MAR-1994 04-APR-1994 AIDS; ss. AAT56332; AAT5633

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enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha manNa at the nucleotide base position indicated in the DE line. Regions of the mENA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit TNF-alpha expression, making them potentially useful for treating rheumatoid archritis, septic shock and other inflammatory disorders including psoriasis, as well as
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94US-0227958.
94US-0228041.
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94US-0291932.
94US-0291433.
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94US-0201109.
94US-0218934.
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94US-0293520.
94US-0300000.
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94US-0311486.
94US-0311749.
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(first entry)
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14-MAY-1997
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Human TNF-alpha hammerhead ribozyme target sequence (nt position 1270).
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Sweedler D;
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                              94US-0316771.
94US-031999.
94US-0321993.
94US-0337608.
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{first entry}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-351090/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for treatment of
28-SEP-1994;
03-OCT-1994;
07-OCT-1994;
11-OCT-1994;
                                                                                                                                                                                               28-NOV-1994;
16-DEC-1994;
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25-MAR-1997
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Matches
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schultz143-3.rng

(updated)
(first entry)

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AAT55815 standard; RNA; 15 BP.
                                                                          25-MAR-2003
25-MAR-1997
                                                        AAT55815;
                  RESULT 241
AATSS815
                                      Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Stinm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA; Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D; Thompson JD, Tracz D, Usman N, Wincet FB, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a preferred target sequence for an enzymatic mucleic acid (i.e. a ribozyme) which cleaves TNF-alpha mRNA at the mucleotide base position indicated in the DE line.
Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis.
Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit TNF alpha expression, making them potentially useful for treating rheumatoid arthritis, septic shock and other inflammatory disorders including psoriassis, as well as
                                                                                                                                                                                                                                                                                                                                                                                                                         Ribozymes having modified bases and methods for producing them for use in inhibiting disease related genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 243; 407pp; English
                                                                                94US-0201109
94US-0218934
94US-0224483
94US-0224483
94US-0227958
94US-0228041
94US-021932
94US-0291932
94US-0291632
94US-0292620
94US-0308039
94US-0311749
94US-0311749
94US-0311749
94US-0311749
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940S-0334847.
940S-0337608.
940S-0345516.
940S-0357577.
                                                       95WO-IB00156
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment of AIDS
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-351090/45.
                                                                                                                                                  06-JUL-1994;
15-AUG-1994;
16-AUG-1994;
17-AUG-1994;
19-AUG-1994;
02-SEP-1994;
Homo sapiens
                 W09523225-A2
                                                                                                                                                                                                                                        28-SBP-1994;
03-OCT-1994;
07-OCT-1994;
                                                       23 - FEB-1995;
                                                                                                                                                                                                                                                                                                                   23-DEC-1994;
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                                    31-AUG-1995
                                                                                                                                 15-APR-1994
18-MAY-1994
                                                                                                                                                                                                                     3-SEP-1994
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Human TNF-alpha hammerhead ribozyme target sequence (nt position 1272).
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                                            Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interlevien 5; 11-5; [70M-1; intercellular adheaton molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; TRF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; ernsuplant rejection; theumatoid arthritis; portiadis; myocardial inchancid arthritis; portiadis; pupocardial isochaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ribozymes having modified bases and methods for producing them for use in inhibiting disease related genes
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94US-0228041.
94US-0245736.
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94US-0291932.
94US-0291433.
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94US-0300000.
94US-0303039.
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94US-0222795.
94US-0224483.
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94US-0337608.
94US-0345516.
94US-0357577.
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94US-0319492
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15-APR-1994;
18-MAY-1994;
06-JUL-1994;
15-AUG-1994;
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19-AUG-1994;
02-SEP-1994;
08-SEP-1994;
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23-SEP-1994;
28-SEP-1994;
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07-0CF-1994;
11-0CF-1994;
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10-NOV-1994;
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Gaps

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1039 ATTIATTATTATGT 1053

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AUTOAUTACOUAUTO 15

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      The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves TMR-alpha mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme alterway sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit TMF-alpha expression, making them potentially useful for treating rheumatoid arthritis, septic shock and other inflammatory disorders including psoriasis, as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bnzymatic nucleic acid, ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TWF-alpha; respiratory syrcytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psortasis; myocardial ischaemia; Rawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS; ss.
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                                                                                                                                                                                                                                              Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
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94US-0245736
94US-0241932
94US-0291433.
94US-0292620
94US-0292620
94US-0303039.
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1 UUAUUAUUUAUUUAU 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (updated)
(first entry)
                                                                                                                                                                                                                                                                                           Local Similarity 26.73
                                                                                                                                                                                                   treatment of AIDS
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25-MAR-1997
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29-MAR-1994
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AAT55817
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Human TNF-alpha hammerhead ribozyme target sequence (nt position 1274).
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Regions of the manh that do not form secondary folding structures and that contain potential hammerhead and hairpin informate cleavage sites were identified by computer analysis.

Tibozymes directed against these manh sequences were designed and shows directed against these manhs sequences were designed and synthesised with modifications that improve their nuclease synthesised with modifications that improve the target sequences and thereby inhibit TNF-alpha expression, making them cequences and thereby inhibit TNF-alpha expression, making them potentially useful for treating rheumatoid arthritis, septic shock and other inflammatory disorders including psoriasis, as well as for treatment of AIDS.

(Cupdated on 25-MAR-2003 to correct PI field.)
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                                                                                                                                                                                                                                                                                    Mcswiggen JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bnzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chromic myelogenous leukaemia; CML; cancer; philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriaals; myocardial ischaemia; Rawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.1%; Score 13.4; DB 1; Length 15;
Best Local Similarity 26.7%; Pred. No. 2.9e+02;
Matches 4; Conservative 10; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1042 TATTATTATGTATT 1056
                94US-0311749.
94US-0314397.
94US-0319492.
94US-0321993.
94US-0334847.
94US-0334847.
94US-0345516.
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(first entry)
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23-SEP-1994;
23-SEP-1994;
28-SEP-1994;
03-OCT-1994;
11-OCT-1994;
04-NOV-1994;
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25-MAR-1997
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Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW, Stinm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA, Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D; Thompson JD, Tracz D, Osman N, Wincott FE, Woolf F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves TWR-alpha mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis Ribozymes directed against these tRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the trarget sequences and thereby inhibit TWF-alpha expression, making them potentially useful for treating rheumatoid arthritis, septic shock and other inflammatory disorders including psoriasis, as well as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1%; Score 13.4; DB 1; Length 15; 26.7%; Pred. No. 2.9e+02; tive 10; Mismatches 1; Indels
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                                                                                                                                             9405-0201109
9405-0201109
9405-0218934
9405-0224483
9405-0227958
9405-0227958
9405-0221932
9405-0291932
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9405-0301939
9405-0301486
9405-031486
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9405-031486
9405-031993
9405-031893
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94US-0363233
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                           Homo sapiens.
                                                   WO9523225-A2
                                                                                                         23-PEB-1995;
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23-SEP-1994;
23-SEP-1994;
                                                                               31-AUG-1995.
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04-NOV-1994
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 AIDS; 88.
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Human TNF-alpha hammerhead ribozyme target sequence (nt position 1259).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Grimm S, Karpeisky A, Kisich K, Maculic-adamic J, Mcswiggen JA; Modak A, Pavco P, Beigleman I, Sullivan SM, Sweedler D; Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
                                                                                                                    gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TMF-alpa; respiratory synctial virus; RSV; bor-abl; oncogene; translocation; chromic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; artherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodefliciency virus; acquired immune defliciency syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribozymes having modified bases and methods for producing them for use in inhibiting disease related genes
                                                                                                            Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
AATS5797 standard, RNA, 15 BP
                                                                                                                                                                                                                                                                                                                                                                                            94US-0222795.
94US-022795.
94US-0227958.
94US-0228041.
94US-021280.
94US-0211280.
94US-0211280.
94US-0292620.
94US-0203520.
94US-0303039.
94US-03103039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              940S-0316771
940S-0319492
940S-031993-
940S-0337608-
940S-0345516-
940S-0365577-
940S-03652377-
                                              (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-351090/45.
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02-SEP-1994;
08-SEP-1994;
23-SEP-1994;
23-SEP-1994;
28-SEP-1994;
                                             25-MAR-2003
25-MAR-1997
                                                                                                                                                                                                                                                                                   #09523225-A2
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07-APR-1994;
15-APR-1994;
15-APR-1994;
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16-AUG-1994;
17-AUG-1994;
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07-0CT-1994;
11-0CT-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-NOV-1994
                                                                                                                                                                                                                                    AIDS; 88.
                       AAT55797;
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1043 ATTATTTATGTATTT 1057

Conservative

Best Local Similarity Matches 4; Conserva

Query Match

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Gaps

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RESULT 246
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                                                                                                                                                                                                                                                                                                                                                                                                                            Human TNF-alpha hammerhead ribozyme target sequence (nt position 1261).
                                                                                                                                                                                                                                               Gaps
                           The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNR-alpha maRNA at the nuclectide base position indicated in the DE line. Regions of the maRNA that do not form secondary folding structures and that contain potential harmerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozyme cleavage sites were identified by computer analysis. Synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit TNR-alpha expression, making them potentially useful for treating rheumatoid arthritis, septic shock and other inflammatory disorders including psoriasis, as well as for treatment of AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition, gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virue; RSV; borr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atheroselerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawaeaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
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                                                                                                                                                                                                                      1.1%; Score 13.4; DB 1; Length 15; 26.7%; Pred. No. 2.9e+02; tive 10; Mismatches 1; Indels
                                                                                                                                                                             (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                 Seguence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
           Claim 2; Page 243; 407pp; English.
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                                                                                                                                                                                                                                                                     1039 ATTTATTATTATGT 1053
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94US-0218934-
94US-0222795-
94US-022795-
94US-0227958-
94US-0228041-
94US-024736-
94US-024736-
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94US-0292620.
94US-0293520.
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1 AUTUAUUAUUAUUU 15
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                                                                                                                                                                                                                                                                                                                                                  AAT55799 standard; RNA; 15
                                                                                                                                                                                                                                                                                                                                                                                             (updated)
(first entry)
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                 Local Similarity
les 4; Conserv
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25-MAR-1997
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15-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIDS; ss.
                                                                                                                                                                                                                                                                                                                                                                        AAT55799;
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Matches
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Human TNF-alpha hammerhead ribozyme target sequence (nt position 1262).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ic J, Mcswiggen JA;
Sweedler D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNP-alpha mRNA at the nucleotide base position indicated in the DB line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit TNF-alpha expression, making them potentially useful for treating rheumatoid arthritis, septic shock and other inflammatory disorders including psoriasis, as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bnzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; INP-alpha; respiratory syncytial virus; RSV; bor-abl; oncogene; translocation; chromic myelogenous leukaemia; CML; cancer; philadelphia chromosome; inflammation; autoimmune disease; atheroscierosis; myecardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dudycz LW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Grimm S, Karpeisky A, Kislich K, Matulic-adamic J, Godak A, Pavco P, Beigleman L, Sullivan SM, Swei Thompson JD, Tracz D, Usman N, Wincott FE, Wooll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 243; 407pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                멾.
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94US-0300000.
94US-03011486.
94US-0311749.
94US-0311749.
94US-0314397.
94US-0319492.
94US-0321993.
94US-0321993.
94US-034647.
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                                                                                                                                                                                                                                                                                                                      94US-0357577
94US-0363233
                                                                                                                                                                                                                                                                                                                                                                                                            (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATS5801 standard; RNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 26.7%
es 4; Conservative
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-351090/45.
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                                                                                                               28-SEP-1994;
03-OCT-1994;
07-OCT-1994;
11-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                     23-DEC-1994;
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25-MAR-1997
                                                                                                                                                                                                                                     04-NOV-1994
                                                                                                                                                                                                                                                                    10-NOV-1994
                                                                                                                                                                                                                                                                                          28-NOV-1994
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Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Grimm S, Karpeißky A, Kisich K, Matulic-adamic J, Mcswiggen JA; Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D; Thompson JD, Tracz D, Usman N, Wincott FB, Woolf T;
myocardial ischaemia; Kawasaki disease; septic shock; HIV;
human immunodeficiency virus; acquired immune deficiency syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 243; 407pp; English.
                                                                                                                                                                                                     94US-0300000.
94US-0303039.
94US-0311486.
94US-0311749.
94US-0314397.
                                                                                                      94US-0201109
94US-0201109
94US-022498
94US-0224483
94US-0227958
94US-02271280
94US-0271280
94US-0271280
94US-0291932
94US-029183
                                                                                                                                                                                                                                                    94US-0319492.
94US-0334847.
94US-0334847.
94US-0345516.
94US-0345516.
94US-0363233.
                                                                                95WO-IB00156
                                                                                                                                                                                                                                                                                                                      (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-351090/45.
                                 Homo saplens
                                                W09523225-A2
                                                                                                                                                                              16-AUG-1994;
17-AUG-1994;
19-AUG-1994;
                                                                                                                                                                                                                                                              11-OCT-1994;
04-NOV-1994;
10-NOV-1994;
                                                                                23-FEB-1995;
                                                                                                                                                                                                                       23-SEP-1994;
23-SEP-1994;
                                                                 31-AUG-1995
                                                                                                30-JAN-1995
                                                                                                                       04-APR-1994
                                                                                                                                       15-APR-1994
                                                                                                                                                                                                       02-SEP-1994;
                                                                                                                                                                                                                 SBP-1994
                                                                                                                                                                                                                                        28-SEP-1994
                                                                                                                                                                                                                                                       07-OCT-1994
                                                                                                        23-FEB-1994
29-MAR-1994
                                                                                                                                                                        -AUG-1994
                 AIDS; 88.
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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential harmerhead and hairpin. Thosymes cleaves and that contain potential harmerhead and hairpin. Ribozymes directed against these mRNA sequences were designed asynthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit TNF-alpha expression, making them potentially useful for treating rheumatoid architis, septic shock and other inflammatory disorders including psoriasis, as well as
Ribozymes having modified bases and methods for producing them for use in inhibiting disease related genes
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RESULT 248
AAT40327/c
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                                                                 1.1%; Score 13.4; DB 1; Length 15; 26.7%; Pred. No. 2.9e+02; tive 10; Mismatches 1; Indels
                              Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;
                                                             Query Match
Best Local Similarity
Matches 4; Conservat
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1047 TITATITATIT 1061

TTATTATTT 15

14

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Gaps

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Conservative

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The sequences given in AAT40324-26 represent primer sequences that
were used to optimise DNA cleavage activity of the enzymatic RNA
molecule of the invention. Primer la hybridises to the 3' portion
of the substrate that becomes attached to the 3' end of the ribozyme.

Primer 1b hybridises to the 3' portion of the ribozyme when no substrate
or product remains attached. Primer 2 hybridises to the 3' end of the
resulting cDNA and introduces the 77 promoter sequence. The self-
splicing group I introm of the invention is based on the large ribosomal
RNA precursor from Tetrahymena thermophila. The biological function of
this molecule is to catalyse its own excision from precursor RNA, to
produce mature RNA. The Tetrahymena wild type sequence was used in
the design of the enzymatic RNA molecules of the invention. A number
of mutations are listed in the specification which improve the enzymatic
properties of this molecule, e.g. G444A, G191U, U190A and A314G. The
modified enzymatic molecules may be used as medical or pharmaceutical
agents for use in anti-viral agents, food products, personal care
                                                                                                                                                                                                                                                                          Wild type; self-splicing group I intron; large ribosomal RNA precursor; Tetrahymena thermophila; catalysis; enzymatic RNA; food product; anti-viral agent; mutation; personal care product; cleaning agent; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enzymatic RNA molecules having one or more point mutation(s) improve the enzymatic performance of the molecules.
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                                                                                                                                                                                                                                          Primer la used to optimise DNA cleavage of a ribozyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15 BP; 3 A; 0 C; 0 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 96; 209pp; English.
1042 TATTATTTATGTATT 1056
                                                                                                                               AAT40324 standard; DNA; 15 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              products or cleaning agents.
                     1 UAUWAUWAUWAWW 15
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Best Local Similarity 93.3:
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-010936/01.
                                                                                                                                                                                                                                                                                                                                                                                           W09531551-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1994;
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                                                                                                                                                                                                      05-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                 23-NOV-1995
                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                   AAT40324;
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                                                                                         RESULT 247
                                                                                                             AAT4032
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KM31-7; glutathione reducing protein; nuclear inclusion a;
protease; autolysis; protein fusion; cleavage; chloroindophenol;
oxidative stress; activated oxygen; therapy; probe; ss.
                                                                                                                                                                                                                                                                        Kawashima I, Koishi R, Serizawa N,
                                                                                                                                                                                                                                              (SANY ) SANKYO CO LTD
                                                                                                                                                                                                                                                                                                WPI; 1996-117338/13.
                                                                                                                                                                                      07-DEC-1994;
13-JUL-1994;
13-SEP-1994;
                                                                                                                                                            13-JUL-1995;
Probe ATT-3
                                                                                                        AU9524970-A.
                                                                                                                                    25-JAN-1996
                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 250
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences given in AAT40327-30 represent sequences that were used to optimise DNA cleavage activity of the enzymatic RNA molecule of the invention. The 3' potion of the substrate was transferred to the 3' terminal G of the ribozyme and amplification was performed. The product of the reaction was a molecule which contained the 3' portion of the substrate attached to the 3' end of the ribozyme. Selection occurred when a primer was hybridised across the ligation junction and used to initiate cDNA synthesis. The primer does not bind to unreacted starting materials and thus led to selective amplification of the catalytically active RNA; a The self-splicing group I intro of the invention is based on the large riboscal RNA precursor from Tetrahymena thermophila. The biological function of this molecule is to catalyse its own excision from precursor RNA to produce mature rRNA. The Tetrahymena wild type envention. A number of mutations are listed in the specification which improve the enzymatic properties of this molecule, e.g. G444A, G191U, U190A and A314G. The modified enzymatic molecules, e.g. G444A, G191U, products, personal care products or cleaning agents, food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                        Wild type; self-splicing group I intron; large ribosomal RNA precursor; Tetrahymena thermophila; catalysis; enzymatic RNA; food product; anti-viral agent; mutation; personal care product; cleaning agent; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                Enzymatic RNA molecules having one or more point mutation(s) improve the enzymatic performance of the molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%; Score 13.4; DB 1; Length 15; 33.3%; Pred. No. 2.9e+02; ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 12 A; 0 C; 0 G; 3 T; 0 other;
                                                                                 Group I intron substrate 3' portion.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 97; 209pp; English.
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                                                                                                                                                                                                                                                                        94US-0270180.
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TTTATTTATTTT 1
 AAT40327 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                (SCRI ) SCRIPPS RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-010936/01.
                                                                                                                                                                                           W09531551-A1.
                                                       05-DEC-1996
                                                                                                                                                                                                                                               26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAY-1996
                                                                                                                                                                                                                                                                         01-JUL-1994;
                                                                                                                                                                                                                                                                                      13-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                     23-NOV-1995
                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                          Joyce GF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT16099;
                             AAT40327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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ID AAT1
XX
AC AAT1
XX
DT 15-M
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Takahashi T;

94JP-0303809. 94JP-0161053. 94JP-0218392.

95AU-0024970.

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                                                                                                                                            DNA probe AIT-3 (AAT16099) is complementary to the AUUUA motif common to the 3' non-translated region of cytokine mRNAs. It was used to screen a cDNA library prepd. From human bone marrow stromal KM-102 cells. A cDNA sequence (AAT16092) coding for a novel dichloroindophenol- and glutathiona-reducing protein, KM11-7 (AAR92050), was obtd. This can be used to treat diseases related to oxidative stress or caused by activated oxygen.
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Clover yellow vein virus nuclear inclusion and dischlorosindophenol or oxidised glutathione reducing protein - useful in autolyshing fusion protein expression systems and for treating diseases related to oxidative stress, or caused by activated oxygen, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                  1.1%; Score 13.4; DB 1; Length 15; 93.3%; Pred. No. 2.9e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                         Sequence 15 BP; 11 A; 0 C; 0 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer la for tetrahymena ribozyme L-21
                                                                                                            Example 3; Page 87; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1044 TTATTTATGTATTTA 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US12394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV09042 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               14; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         retrahymena sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9802583-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JAN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15
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This sequence is a primer for a wild type tetrahymena ribozyme L-21 form.

The amplified sequence is an example of a catalytic RNA (1) of the invention, which catalyses site-specific cleavage of nucleic acid under physiological conditions includes a sequence derived from a group I bysiological conditions includes a sequence derived from a group I intron. Similar catalytic RNAs (II) which catalyse hydrolysis of amide can are useful as peptidases and proteases, e.g. in wound debridement, clot dissolution, in detergents or as a meat tenderiser. (I) cleave single- and (partly) double-stranded nucleic acids in vitro or in vivo, and are potentially useful as antiviral agents and gene regulators; also to generate defective but still immunogenic viruses (for vaccines); clagmostically to detect mutations in nucleic acid or to identify nucleic acid binding agents; to modulate/terminate reactions initiated by DNA primers; to generate truncated transcripts from DNA; to modulate therapeutic/diagnostic processes using antisense sequences; in DNA in vitro evolution processes that provide better catalytic performance; broader active temperature and pit ranges; new enzymatic activities or specificities; altered recognition sites or co-factor requirement.
                                                                                                                                                                                                Catalytic RNA for site-specific cleavage of nucleic acid or hydrolysis of amide bonds - and ribozyme amidase intermediates, useful e.g. as peptidase(s), antiviral agents and gene regulators
                                                                                                                                                                                                                                                                                                       Example 1; Page 90; 215pp; English
96US-0682423
                                              (SCRI ) SCRIPPS RES INST.
                                                                                                                                                  WPI; 1998-110627/10
17-JUL-1996;
                                                                                                 Joyce GF;
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Gaps ö 1.1%; Score 13.4; DB 1; Length 15; 93.3%; Pred. No. 2.96+02; ative 0; Mismatches 1; Indels Sequence 15 BP; 3 A; 0 C; 0 G; 12 T; 0 other; Query Match Best Local Similarity 93.3 Matches 14; Conservative

1047 TITATGRATITY 1061 1 TTATTTATTTATT 15 ઠે 윰

AAH26597 standard; mRNA; 15 RESULT 251 AAH26597

AAH26597;

12-NOV-2001 (first entry)

Human interferon-alpha gene 3' UTR AU-rich element.

Interferon-alpha; human; AU-rich element;

Homo sapiens

/*tag= b /note= "AUUUA motif" 10..14 /*tag= c /note= "AUUA motif" a "AUUUA motif" Location/Qualifiers *tag= 'note= misc_feature misc_feature misc_feature

WO200164921-A1

07-SEP-2001.

28-FEB-2001; 2001WO-US06782

29-FEB-2000; 2000US-0515369.

(UYCO) UNIV COLUMBIA NEW YORK

isher PB, Madireddi MT;

WPI; 2001-565508/63.

Melanoma differentiation associated gene-7 promoter capable of treating cancer comprises directing transcription of heterologous coding sequence encoding tumour suppressor polypeptide positioned downstream, useful for treating cancer -

Disclosure; Fig 2C; 132pp; English.

The present sequence is that of an AU-rich sequence in the 3' untranslated region (3'UTR) of human interferon-alpha mRNA. The presence of AU-rich elements (ARSB) in eukaryotic mRNAs. The presence of AU-rich elements (ARSB) in eukaryotic mRNAs correlates with rapid mRNA turnover and post-translational control. The ARB consists of multiple AUUNA motifs or sequences resembling it. A sufficientiation associated gene-7 (Mda-7) gene (see AAH26596). The invention provides recombinant expression constructs in which the human Mda-7 promoter (see AAH36595) is operably linked to a coding sequence encoding a tumour suppressor protein. Sparascian construct is used in a claimed method of treating melanoma, construct is used in a claimed method of treating melanoma, neuroblastoma, astrocytoma, glioblastoma multiforme, cervical cancer, breast cancer, octonaryous system.

Sequence 15 BP; 5 A; 0 C; 0 G; 10 U; 0 other;

Gaps ö 1.1%; Score 13.4; DB 1; Length 15; 33.3%; Pred. No. 2.9e+02; ve 9; Mismatches 1; Indels Best Local Similarity 33.3%; Matches 5; Conservative Query Match

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RESULT 252 AAF80978

AAF80978 standard; DNA; 15 BP AAF80978;

(first entry) 32-MAY-2001

Human, prostaglandin-endoperoxide synthase 2, PTGS2, cyclooxygenase 2, single nucleotide polymorphism; SNP; immune-related disorder; arthritis; inflammation; PCR primer; ss. PTGS2 allele specific oligonucleotide primer SEQ ID 84.

Homo sapiens

WO200107662-A1.

01-FEB-2001.

24-JUL-2000; 2000WO-US20114.

99US-0145170. 22-JUL-1999;

(GENA-) GENAISSANCE PHARM INC.

Denton RR, Nandabalan K, Sanchis A, Stephens JC,

Tanguay DA;

#PI; 2001-182805/18.

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(MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                               AAF48964 standard; DNA; 15 BP
                                                                                                                                                                                                                                99US-0140345.
                                                                                                                                                                                                                         21-JUN-2000; 2000WO-AU00693
                                                                                                         Query Match
Best Local Similarity 93.39
Matches 14; Conservative
                                                                                                                                                                                                             WO200078341-A1
                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                21-JUN-1999;
                                                                                                                                                            30-MAR-2001
                                                                                                                                                                                                                   28-DEC-2000.
                                                                                                                                                     AAF48964;
         haplotype
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Werther GA,
                                                         WPI; 2001-041421/05.
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      Wraight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            쉽
                                                                                                                                                                                                   This invention relates to a polynucleotide sequence that is a polymorphic variant of the human prostaglandin-endoperoxide synthase 2 (PTGS2) gene also referred to as cyclooxygenase 2. The human PTGS2 gene sequence also referred to as cyclooxygenase 2. The human PTGS2 gene sequence.

AAP80895 contains 27 single mucleotide polymorphisms (SNPB). AAP80896 and AAP80897 represented by AAB72199. The invention includes PCR and contains in represented by AAB72199. The invention includes PCR and probes represented in AAP80898 - AAF81151 which are used to isolated and characterise the PTGS2 gene sequence, and to locate the positions of the SNPB. PTGS2 proteins and plymich of care used to express variant PTGS2 proteins, for structural analysis or drug-binding studies and also in gene therapy (either carpies) in progness, progness and also in gene therapy (either carpies) progness and unbit of sead against PTGS2 are expressing PTGS2 or inhibitory RNA). Antibodies raised against PTGS2 are known, polymorphisms and used to determine PTGS2 haplotype and genotype, consetul for diagnosis, prognesis and therapy and analysis of the new, and known, polymorphisms and used to determine PTGS2 but also disease for a succeptibility, severity or stage. Anti-PTGS2 antibodies are particularly cused for developing diagnostic tests and treatments for immune-related disorders such as arthritis and inflammation. The polymorphisms may also the used to study expression and biological function of PTGS2 ranageming affects of the service of the present of the progressing and testing, and for assessing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; shin disporate; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichbyosis; serborrhoea; ruba; keatoolsis, neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition; hyperplasia; kidney disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                      New nucleic acid containing polymorphisms in the cyclooxygenase-2 ge for gene therapy of inflammation and for establishing a genotype or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1%; Score 13.4; DB 1; Length 15; 33.3%; Pred. No. 2.9e+02; ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 15 BP; 4 A; 0 C; 0 G; 11 T; 0 other;
                                                                                                                                                                Disclosure; Page 23; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         effects of therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGFBP3 oligonucleotide #2384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1045 TATTIATGIATITAT 1059
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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Pactor [IGF]-1 inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be useful of sequence is an oligonucleotide which can be useful for ameliorating the effects of AAF4515-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityridasis, ruba, pilaris, serborthoea, keloids, keratosis, neoplasas, scleroderma, warts, benign growths, cancers of the skin, a hyperneovasquiar condition such as a neovascular condition of the method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense therapy, antiproliferative, antiinflammatory; antipsoriatic; cytostatic; dermatological, cardiant; virucide; ophthalmological, keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; prowth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hypernecvascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia.
                                                                                                                      antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                           Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antison nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 93.3%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15 BP; 3 A; 2 C; 0 G; 10 T; 0 other;
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Edmondson SR;
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                                                                                                                                                                                                                       Example 7; Page 59; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUN-2000; 2000WO-AU00693.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-041421/05
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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligomucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP], which is capable of inhibiting or reducing growth factor mediated cell proliferation, inhibiting or reducing growth factor mediated cell proliferation, oligomucleotide which can be used to design the antisense oligomucleotide which can be used to design the antisense oligomucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborthoea, keloids, keratosis, neoplasias, scleroderma, warts, bengan growths, cancers of the retina, brain or skin, growth factor-mediated malignancies, other retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of
Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               blood vessels or any other hyperplasia.
                                                                                                                                              Example 7; Page 59; 201pp; English.
                                                                                      inflammation
                                                                                   proliferation and/or
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Sequence 15 BP; 3 A; 1 C; 0 G; 11 T; 0 other;

Gaps ö 1.1%; Score 13.4; DB 1; Length 15; 93.3%; Pred. No. 2.9e+02; Live 0; Mismatches 1; Indels 14; Conservative Query Match Best Local Similarity Matches 14; Conserv

TITATATITITAACI 1535 1521

8 셤 AAF48966 standard; DNA; 15

AAF48966;

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(first entry) 30-MAR-2001

IGFBP3 oligonucleotide #2386.

Antisense therapy, antiproliferative, antinflammatory, antipsoriatic, cytostatic, dermatological; cardiant; virucide, ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; piraris; growth factor mediated cell proliferation; ichthyosis; serborinoea; ruba; keatosis; ineoplasia; scoleroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasis, kidney disease; neovascular condition of the retina; ss. APRA8966
ANC AAP4896
XX AAP4896
XX AAP4896
XX AAP4899
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XX AAP489

Homo sapiens

WO200078341-A1.

28-DEC-2000.

21-JUN-2000; 2000WO-AU00693

99US-0140345.

21-JUN-1999;

(MURD-) MURDOCH CHILDRENS RES INST.

Edmondson SR;

ą,

Werther

Wraight CJ,

WPI; 2001-041421/05.

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Givoth Factor [IGRP-].

Cartisense oligonucleotide, (for Insulin-like Givoth Factor [IGRP-].

Creeptor, IGF binding protein [IGFBP-]. Or IGFBP-], which is capable of inhibiting or reducing growth factor mediated cell proliferation, coligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the affects of psoriasis, ichthyosis, pityriasis, ruba, plairis, serborrhoea, keloids, keratosis, neoplasias, soleroderma, warts, benign growths, cancers of the skin, a hypernevascular condition of the retina, brain or skin, growth factor-mediated malignancies, other scherotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 1.1%; Score 13.4; DB 1; Length 15; Similarity 93.3%; Pred. No. 2.9e+02; 4; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15 BP; 3 A; 1 C; 0 G; 11 T; 0 other;
                         Example 7; Page 59; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1522 TTATATTTTAACTT 1536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Antisense therapy, antiproliferative, antiinflammatory, antipsoriatic, cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; gath disorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFB-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; sclaroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia, kidney disease; neovascular condition of the retina; ss. IGFBP3 oligonucleotide #2387. AAPF48967
AAPF48967
AAPF48967
AAPF4
AAPF48967
AAPF4
AAPF48967
AAPF4
AAPF48967
AAPF4
AAPF48967
AA

BP

AAF48967 standard; DNA; 15

(first entry)

30-MAR-2001 AAP48967;

domo sapiens

WO200078341-A1

99US-0140345. 21-JUN-1999;

21-JUN-2000; 2000MO-AU00693

(MURD-) MURDOCH CHILDRENS RES INST.

Edmondson Wraight CJ, Werther GA,

SR;

WPI; 2001-041421/05

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation -

Sxample 7; Page 59; 201pp; English.

The present invention relates to a method for ameliorating the

A314G. The modified enzymatic molecules may be used as medical or pharmaceutical agents for use in anti-viral agents, food products, personal care products or cleaning agents.

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Gaps

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Length 16;

tch 1.1%; Score 13.4; DB 1; Length 1 al Similarity 93.3%; Pred. No. 3.1e+02; 14; Conservative 0; Mismatches 1; Indels

Query Match Best Local Matches

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Sequence 16 BP; 13 A; 0 C; 0 G; 3 T; 0 other;

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antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be useful for amaliorating the effects of AAF45151 and AAF45151-R45161. The method is useful for amaliorating the effects of keratosis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, canners of the skin, a hyperneovascular condition such as a neovascular condition of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAT4031-32 represent sequences that were as substrate molecules in experiments for selection of improved catalytic activity of riboxymes. The evolution experiment spanned 10 successive generations and catalytic activity was deduced after each generation. The self-splicing group I intron of the invention is based on the large function of this molecule is to catalyse its own excision from precursor rRNA to produce mature rRNA. The Tetrahymena wild type sequence was used in the design of the enzymatic RNA molecules of the invention. A number of mutations are listed in the specification which improve the enzymatic properties of this molecule, e.g. G444A, G191U, U190A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wild type; self-splicing group I intron; large ribosomal RNA precursor; Tetrahymena thermophila; catalysis; enzymatic RNA; food product; anti-viral agent; mutation; personal care product; cleaning agent; ss.
                                                                                                                                                                                                                 retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA cleavage substrate #2 for generation of improved ribozymes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enzymatic RNA molecules having one or more point mutation(s) improve the enzymatic performance of the molecules.
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 93.3%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                    Sequence 15 BP; 3 A; 1 C; 0 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 111; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        1523 TATATTTTAACTTT 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332/c
AAT40332 standard; DNA; 16 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-0270180.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TATTTTTTAACTTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-DEC-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-010936/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1994;
13-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-NOV-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Joyce GF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT40332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 257
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The sequences given in AAT40327-30 represent sequences that were used to optimise DNA cleavage activity of the enzymatic RNA molecule of the optimise DNA cleavage activity of the enzymatic RNA molecule of the invention. The 3' potion of the substrate was transferred to the 3' terminal Go of the ribozyme and amplification was performed. The product of the reaction was a molecule which connained the 3' portion of the substrate attached to the 3' end of the ribozyme. Selection occurred when a primer was hybridised across the ligation junction and used to initiate cDNA synthesis. The primer does not bind to unreacted starting materials and thus led to selective amplification of the invention is based on the large ribosomal RNA precursor from Tetrahymena thermophila. The biological function of this molecule is to catalytically crive precursor RNA to produce materials for the arranymena wild type sequence was used in the design of the enzymatic RNA molecules of the invention. A number of mutations are listed in the specification which invention. A number of mutations are listed in the specification which inspond and A314G. The modified enzymatic molecule, e.g. G444A, G191U, U190A and A314G. The modified enzymatic molecules may be used as medical or pharmaceutical agents for use in anti-viral agents, food products, personal care products or cleaning agents.
                                                                                                                                                                                                                                                                               wild type; self-splicing group I intron; large ribosomal RNA precursor; Terrahymena thermophila; catalysis; enzymatic RNA; food product; anti-viral agent; mutation; personal care product; cleaning agent; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enzymatic RNA molecules having one or more point mutation(s) improve the enzymatic performance of the molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16 BP; 3 A; 1 C; 0 G; 12 T; 0 other;
                                                                                                                                                                                                                                                 Improved cleavage group I intron primer 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 98; 209pp; English
                                                                                                                                  AAT40329 standard; DNA; 16 BP
1047 TITATETATITY 1061
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                      15 TTATTATTATT 1
                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-010936/01.
                                                                                                                                                                                                                                                                                                                                                                                                          WO9531551-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1994;
13-MAY-1994;
                                                                                                                                                                                                              05-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Joyce GF;
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TITATITATITA 15

Length 16;

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AAC65598 standard; DNA; 16
                                                                                                     AAC65598;
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                                           RESULT 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is a primer for a wild type tetrahymena ribozyme I-21 form. The amplified sequence is an example of a catalytic RNA [1] of the cinvention, which catalyses site specific cleavage of muclaic acid under physiological conditions includes a sequence derived from a group I intron. Similar catalytic RNAS [1] which catalyse hydrolysis of amide cands are useful as peptidases and proteases, e.g. in wound debridement, clot dissolution, in detergents or as a meat tenderiser. [1] cleave single- and (partly) double-stranded nucleic acids in vitro or in vivo, and are potentially useful as antiviral agents and gene regulators; also to generate defective but still immunogenic viruses (for vaccines); diagnostically to detect mutations in nucleic acid or to identify nucleic acid binding agents; to modulate/terminate reactions initiated by DNA primers; to generate truncated transcripts from DNA; to modulate truncated transcripts from DNA; to modulate truncated transcripts from DNA; to modulate from processes using antisense sequences; in DNA fingerprinting and for vector construction. [1] and [1] are produced by in vitro evolution processes that provide better catalytic performance; broader active temperature and pH ranges; new enzymatic activities or specificities; altered recognition sites or co-factor requirement.
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                                                                                                                                                                                                                                                                          Tetrahymena ribozyme; group I intron; amide end hydrolysis; peptidase; protease; antiviral agent; gene regulator; immunogenic virus; vaccine; mutation detection; PCR primer; ss.
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Catalytic RNA for site-specific cleavage of nucleic acid or hydrolysis of amide bonds - and ribozyme amidase intermediates, useful e.g. as peptidase(8), antiviral agents and gene regulators
                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.1%; Score 13.4; DB 1; Length 16; Best Local Similarity 93.3%; Pred. No. 3.1e+02; Matches 14; Conservative 0; Mismatches 1; Indel8
                            1; Indels
1.1%; Score 13.4; DB 1; 93.3%; Pred. No. 3.1e+02; ative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16 BP; 3 A; 1 C; 0 G; 12 T; 0 other;
                                                                                                                                                                                                                                                 Primer 1 for tetrahymena ribozyme L-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 92; 215pp; English
                                                                                                                          1047 TITALGIALITATIT 1061
                                                                             1 TTTATTTATTTATT 15
 Query Match
Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                           Mouse; uteroglobin; immunoglobulin A mediated disease; IgA nephropathy; autoimmune disorder; pulmonary inflammation; Wegener's granulomatosus; Goodpasture's disease; diabetic glomerulosclerosis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of a composition comprising uteroglobin (or a fragment, derivative, mimetic or variant), for inhibiting or treating an immunoglobulin-A mediated autoimmune disorders, e.g. diabetic glomerulosclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.1%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humicola grisea glucoamylase hybridization probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16 BP; 1 A; 0 C; 3 G; 12 T; 0 other;
                                                Human uteroglobin SNP PCR primer hUG-3100AF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gxample 12; Page 43; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mukherjee AB, Zheng F, Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1204 ATTARACAAACAAAC 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ78891 standard; DNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-1999; 99US-0130434.
                                                                                                                                                                                                                                                                                                                                                   13-APR-2000; 2000WO-US09979.
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(first entry)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pulmonary inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-687100/67.
                                                                                                                                                                                                                                                   40200062795-A2
                                                                                                                                                                                                   Homo sapiens.
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18-DEC-1995
14-FEB-2001
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1047 TTTATGTATTTATTT 1061

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Gaps

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                                                                                                                                                                                                                                                                                                  The DNA probe and corresponding probes covering the degenerate sites (AAA78885-Q78890) correspond to amino acids 17-22 of the H. grisea glucoamylase peptide GA1 (AAR6293), and are used as hybridization probes to detect and isolate H. grisea glucoamylase DNA in a Southern blot. Resulting genomic DNA fragments are excised and cloned in plasmid pRSH1. This illustrates the main claims of the patent, i.e. a vector containing (i) DNA encoding a neterologous polypeptide (chymosin, prochymosin, preprochymosin, Aspergillus niger glucoamylase, H. grisea glucoamylase, or Mucor miehei carboxyl proteases and (ii) a secretory signal peptide, and a filamentous fungus (Aspergillus, Trichoderma, Neurospora, Podospora, Endothia, Mucor, Cochiobolus or Pyriclaria, especially A. nidulans, A. awamori or T. reesei) transformed with the vector (updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enzyme; bioluminescence; luminescence; label; DNA probe;
                                                                                                                                                                                                                  Vectors and DNA for expressing polypeptide(s) in filamentous fungi-include secretory signal sequences that are native or foreign to heterologous polypeptide(s), such as chymosin or glucoamylase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 1.1%; Score 13.4; DB 1; Length 17; 1 Similarity 93.3%; Pred. No. 3.3e+02; 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                   Lawlis VB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 BP; 11 A; 2 C; 0 G; 3 T; 1 other;
                                                                                                                                                                   Hayenga KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Renilla reniformis luciferase DNA probe-1.
                                                                                                                                                                                                                                                                              Example 9A3; Page 22; 50pp; English.
                                                                                                                                                                   Gray GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ92084 standard; cDNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Luciferase, enzyme, biolumines
antibody; oligonucleotide, ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1047 TETATGRAPHT 1061
                                                                               85US-0771374.
86US-0882224.
86BP-0306624.
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                                                       94EP-0201751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {updated)
(first entry)
                                                                                                                                     (GEMV ) GENENCOR INT INC
                                                                                                                                                                   Cullen D,
                                                                                                                                                                                             WPI; 1994-359750/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-DEC-1993;
                                                       27-AUG-1986;
                                                                                  29-AUG-1985;
                                                                                               07-JUL-1986;
27-AUG-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-DEC-1989;
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07-JAN-1996
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 EP625577-A1
                            23-NOV-1994
                                                                                                                                                                   Berka RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ92084;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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The present sequence represents the preferred target sequence for an ensymatic nucleic acid, especially a hammerhead ribozyme, which cleaves the human c-myb sequence at the base position indicated in the
                                                                                                                                                                                                                                                                                                                                              Gape
                                                                                                                                                                                                 This 17-mer oligomucleotide DNA probe, along with Probe-2 (AAQ92085) are used to screen an R. reniformis cDNA library to isolate cDNA encoding Renilla luciferase. The luciferase was then expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human c-myb hammerhead ribozyme target sequence (nt. position 2712).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New enzymatic nucleic acid molecules - which cleave RNA produced by e.g. c-myb, for treating restenosis or cancer
                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                       New recombinant Renilla luciferase polypeptide - used as a luminescent tag, partic in bio-luminescence assays and for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bnzymatic nucleic acid; hammerhead; ribozyme; cleavage; human;
smooth muscle cell; hyperproliferation; restenosis; cancer;
c-myb; coronary angioplasty; 86.
                                                                                                                                                                                                                                                                                                                   1.1%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 3.3e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stinchcomb DT;
                                                                                                                                                                                                                                                      PF field. >
                                                                                                                                                                                                                                                                                             Sequence 17 BP; 6 A; 0 C; 2 G; 9 T; 0 other;
                                                                                                                                                                                                                                         using B. coll.
(Updated on 25-MAR-2003 to correct
(Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Draper K, Jarvis T, McSwiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 77; 128pp; English.
                                                                                                                                                                              Disclosure; Fig. 4; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                       1259 AAATAATTTTTAGT 1273
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                                                                                                                                                                                                                                                                                                                                                                                      3 AATAATTTTTTGT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 93.33
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-010927/01.
                                                                                                                                                     of antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9531541-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT81505;
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 263
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(UYGE-) UNIV GEORGIA RES FOUND INC

Lorenz WW;

Cormier MJ,

WPI; 1995-199741/26.

92US-0933017. 93US-0079700. 93US-0167650.

20-AUG-1992; 17-JUN-1993; 14-DEC-1993;

Gaps ö

Length 17;

1.1%; Score 13.4; DB 1; ilarity 93.3%; Pred. No. 3.3e+02; Conservative 0; Mismatches 1;

616 ACAAAAAACAACAAA 630

15 ACAAAAAACAAAAA 1

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Sscobedo J, McSwiggen J, Pavco P,
                                                                                                                                                                                                                                                                           Claim 4; Page 173; 218pp; English.
                                                                                                       AAX75068 standard; RNA; 17 BP.
                                                                       1617 AAAATATATATTTGTT 1631
                                                                                                                                                                                                           96US-0584040.
95US-0005974.
                                                                                                                                                                                                  96WO-US174B0.
                                                                                                                                                                                                                        (CHIR ) CHIRON CORP.
(RIBO-) RIBOZYME PHARM INC
                                                                                                                          (first entry)
                                                                                                                                                              foetal liver kinase 1; ss
                                                                             WPI; 1997-259017/23.
                                                                                                                                                                                                   25-0CT-1996;
                                                                                                                                                                                WO9715662-A2
                                                                                                                                                                                                           11-JAN-1996;
                                                                                                                                                                                                                26-OCT-1995;
                                                                                                                          28-JUL-1999
                                                                                                                                                                                         01-MAY-1997.
                                                                                                                 AAX75068
                                                                                                                                                                       Mus sp.
                                                                                                   AAX75068/c
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Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
target sites using a computer folding algorithm, and regions of the mRNA which did not form secondary folding algorithm, and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme cleavage sites were identified. Ribozymes were synthesised and their activities optimised by either varying the length of the binding arms or by modification to prevent degradation by nucleases. The ribozymes cleave the c-myb sequence and can be used to prevent smooth muscle cell hyperproliferation in restenosis, especially after coronary angloplasty, and in cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding i or more receptors of vascular endothelial growth factor (VBGF). A patient (preferally human) having a condition associated with the level of the fms-like tyrosine kinase i (fil-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase I (fik-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAK77275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vascular endothelial growth factor receptor; VBGF receptor; flt-1; flx-1; KDR; hammerhead riboxyme; hairpin riboxyme; oleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular desase; tumour tyrosine kinase 1; kinase insert domain containing receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ō
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stinchcomb D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 8 A; 0 C; 0 G; 9 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 0 A; 0 C; 2 G; 15 U; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VBGF). A patient (preferably human) having a condition associated with the level of the fime-like tyrosine kinase 1 (file-1), kinase insert domain containing receptor (KDR) and/or feetal liver kinase 1 (file-1) (e.g. tumour anglogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the mucleic acid molecule or the expression vector to the patient. AAX6775 to AAX75752 represent specific examples of nucleic acid molecules from the present invention.
                                                                                                                                                      Vascular endothelial growth factor receptor; VBGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesia; psoriamis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinaee 1; kinase insert domain containing receptor; foetal liver kinase 1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                        Human flt1 VEGF receptor hammerhead ribozyme substrate #1330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches 9; Conservative 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stinchcomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 9 A; 2 C; 0 G; 6 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sscobedo J, McSwiggen J, Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 86; 218pp; English
                 AAX70035 standard; RNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                96US-0584040.
95US-0005974.
                                                                                                                                                                                                                                                                                                                                                                              96WO-US17480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AUAAACUCAAAUUUA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR ) CHIRON CORP.
(RIBO-) RIBOZYME PHARM INC.
                                                                                         28-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-259017/23.
                                                                                                                                                                                                                                                                                                         W09715662-A2.
                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                              25-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                  11-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                           01-MAY-1997.
                                                       AAX70035;
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genetic disease; diagnosis; cystic fibrosis; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (YBGF). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (YBR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the mucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention.
                                                                                                     Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor; foetal liver kinase 1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 3.3e+02; tive 0; Mismatches 1; Indels
                                                                                    Human flt1 VEGP receptor hammerhead ribozyme substrate #844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASO 2184dAN wild-type sequence of cystic fibrosis mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multiplex allele-specific diagnostic assay; MASDA; allele-specific oligonucleotide; ASO; polymorphism;
                                                                                                                                                                                                                                                                                                                                            Escobedo J, McSwiggen J, Pavco P, Stinchcomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 7 A; 3 C; 2 G; 5 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 72; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT60263 standard; DNA; 17 BP
                   BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               749 TAGAATGEGATATET 763
                                                                                                                                                                                                                                                                         96US-0584040.
                                                                                                                                                                                                                                                   96WO-US17480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 TAGAATGEGACATET 3
                                                                                                                                                                                                                                                                                                           (CHIR.) CHIRON CORP.
(RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                   AAX69549 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 93.3°
                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-259017/23.
                                                                                                                                                                                                        WO9715662-A2
                                                                                                                                                                                                                                                    35-OCT-1996;
                                                                                                                                                                                                                                                                         11-JAN-1996;
26-OCT-1995;
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                              01-MAY-1997.
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                                                                28-JUL-1999
                                          AAX69549;
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      267
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AAT60263/
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Allele-specific oligonuclectides (ASOs) (AAT60210-41) representing known cystic fibrosis mutations, and corresponding ASOS (AAT60242-70) representing wild-type sequences, are examples of ASOs that can be used in a multiplex allele-specific diagnostic assay (MASDA) that has the capacity to analyse over 500 samples of a large number of mutations (over 100) in a single assay. Target DNA is immobilised to a solid support and interrogated in combinatorial fashion with a mixture of mutation-specific ASOs in solution. The ASO(s) or corresponding to the specific mutation(s) present in the sample is corresponding to the specific mutation(s) present in the sample is corresponding to the specific mutation(s) is identified. MASDA can be used to detect genetic alterations associated with genetic disorders, to identify genetic polymorphisms, to determine the molecular basis of genetic diseases, or for high-resolution of disease-causing microorganisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cyrostatic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; porians; verruca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying genetic alterations or target sequences in nucleic acid samples - useful for detecting genetic alterations associated with a disease, e.g. cystic fibrosis and sickle cell anaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Integrin alpha 6 subunit substrate sequence SEQ ID NO:4431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 1 A; 1 C; 3 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 42; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
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                                                                                                                                                                                                                                                                                                          96WO-US14842.
                                                                                                                                                                                                                              96WO-US14842.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA21205 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         (GENZ ) GENZYME CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-202258/18.
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                                                                                                                                                                                                                              13-SEP-1996;
                                                                                                                                                                                                                                                                                                              13-SEP-1996;
                                                                       WO9710366-A2
                                                                                                                                                       20-MAR-1997.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shuber AP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA21205;
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McSwiggen JA;

Coeshott C,

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The present invention describes enzymatic nucleic acid molecules with RNA clearing activity, which specifically cleave RNA encoded by an aryl RNA clearing activity, which specifically cleave RNA encoded by an aryl gene, an integrin submuit beta 3 gene, an integrin submuit beta 3 gene, an integrin alpha 6 submuit gene, or a Tie-2 gene. AAA16775 to AAA1762 represent ribozyme sequences for AAA1768 represent their corresponding target sequences; AAA19155 to AAA19156 and AAA1768 to AAA19155 and AAA31915 to AAA19155 to AAA19159 represent ribozyme sequences for integrin alpha 6 submuit, and AAA20362 to AAA2130 and AAA21596 to AAA21468 represent ribozyme sequences for integrin alpha 6 submuit, and AAA20362 to AAA2130 and AAA21596 to AAA2150 and AAA2130 to AAA21305 represent ribozyme sequences for integrin submuit beta 3, and AAA21365 represent ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARRY, or are at cancer, diabetic retinopathy, age related mecular degeneration (ARW), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, angiotistome of tuberrous sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, dintegrin submuit alpha-6, or the levels of ARRY, Tie-2, integrin submuit alpha-6, or the levels of ARRY, Tie-2, integrin submuit beta-3.
                                                                                                                                                                                                                                                                                             Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an anglogenic factors
                                                                                                                                                                                                                                                                                                                                                                  Claim 55; Page 193; 305pp; English.
                                                                                                                                                                                                     Jarvie T,
                                                                 99WO-US06507
                                                                                                             9BUS-0079678
                                                                                                                                                            (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                     Roberts E,
                                                                                                                                                                                                                                                    WPI; 1999-591315/50.
                                                                 24-MAR-1999;
                                                                                                             27-MAR-1998;
                     07-OCT-1999.
                                                                                                                                                                                                          Pavco PA,
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Sequence 17 BP; 4 A; 1 C; 2 G; 10 U; 0 other;

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0; Gaps
Match 1.1%; Score 13.4; DB 1; Length 17; Local Similarity 33.3%; Pred. No. 3.3e+02; es 5; Conservative 9; Mismatches 1; Indels
  Query Match
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AAA21206 standard; RNA; 17 BP AAA21206;

RESULT 269

19-JUN-2000 (first entry)

Integrin alpha 6 subunit substrate sequence SEQ ID NO:4432.

Human; aryl hydrocarbon nuclear transport; ARNT; TIB-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; harmerhead ribozyme; angiogenic factor; cytostatic; antidabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inclammation; nevascular glaucoma; myopic degeneration; psoriasis; vertuca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;

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The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl Pydrocarbon nuclear transporter (ARNY) gene, an integrin subunit beta 3 gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA1767 to AAA1765 to AAA1762 represent ribozyme sequences for ARNY, corresponding target sequences; AAA1768 to AAA1968 to AAA2169 to AAA234 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome;
                                                                                                                                                                                                                                                                                                                                                               McSwiggen JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.1%; Score 13.4; DB 1; Length 17; 33.3%; Pred. No. 3.38+02; tive 9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              integrin subunit alpha-6, or integrin subunit beta-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel ribozymes for modulating the synthesis, expresstability of an mRNA encoding an anglogenic factors
                                                                                                                                                                                                                                                                                                                                                             Coeshott C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 4 A; 1 C; 2 G; 10 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 55; Page 193; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                             Jarvis T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1524 ATATTTTAACTTTA 1538
                                                                                                                                                                                                                                                           98US-0079678.
                                                                                                                                                                                                                                                                                                            (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 33.3
Les 5, Conservative
                                                                                                                                                                                                                                                                                                                                                               Roberts B,
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-591315/50.
                                                      Homo sapiens
                                                                                                                                                                                                          24-MAR-1999;
                                                                                                                                                                                                                                                         27-MAR-1998;
                                                                                                      #09950403-A2
                                                                                                                                                          07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                               Pavco PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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RESULT 270

AAA21207 standard; RNA; 17 BP 19-JUN-2000 (first entry) AAA21207; AAA21207
IID AAA3
XX AAA
XX AAA3
XX BAA3
XX I 19-2
XX I IIIte
XX Huma
XX Huma
XX IIITE
XW IIITE
XW HAMM

Human; aryl hydrocarbon nuclear transport; ARNT; TIB-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; Integrin alpha 6 subunit substrate sequence SEQ ID NO:4433.

Integrin alpha 6 subunit substrate sequence SBQ ID NO:4602.

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ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARWD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; or augaris; angiofibroma; tuberous solerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
                                                                                                                                                                                                                               Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors
                                                                                                                                                                                           Jarvis T, Coeshott C, McSwiggen JA;
                                                                                                                                                                                                                                                               Claim 55; Page 193; 305pp; English.
                                                                                                                                 99WO-US06507.
                                                                                                                                                     98US-0079678.
                                                                                                                                                                        (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                            Pavco PA, Roberts E,
                                                                                                                                                                                                              WPI; 1999-591315/50.
                                                                        Homo sapiens
                                                                                           WO9950403-A2
                                                                                                                                 24-MAR-1999;
                                                                                                                                                     27-MAR-1998;
                                                                                                              07-OCT-1999.
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The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl RNA cleaving activity, which specifically cleave RNA encoded by an aryl wide control of the submit gene, or a Tie-2 gene. AAA16775 to AAA17167 and AAA17661 to AAA17622 represent ribozyme sequences for ARNT, and AAA17167 and AAA17168 to AAA196775 to AAA19154 represent ribozyme sequences for Tie-2, and AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA19087 to AAA19223 represent their corresponding target sequences. AAA19223 to AAA21681 represent ribozyme sequences. AAA19223 to AAA21681 represent ribozyme sequences. AAA21689 represent their corresponding target sequences. AAA21689 to AAA21681 represent their corresponding target sequences. AAA21689 to AAA21687 and AAA21689 represent their corresponding target sequences. AAA21689 to AAA21687 represent their corresponding target sequences. AAA21689 to AAA21687 and AAA2263 to AAA21689 to AAA21689 represent their corresponding target sequences. AAA21689 to AAA21689 represent their corresponding target sequences. Ctor integrin subunit beta 3, and AAA22476 to AAA23342. Represent ribozymes of the invention are used for modulating the sequences. The ribozyme sequences capped in subunit beta 3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer. diabetic retinopathy, age related manual degeneration (ARMD), inflammation, and arthritis, as well as neovascular degeneration (ARMD), inflammation, and arthritis, as well as angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber. Syndrome, Kippel-Trenaunay.Weber syndrome, osler-Weber-Remin sphunit alpha-6, or Tie-2, and degeneration granic scheme stains, Sturge Webr. Andath and degeneration (ARMD), inflammation, and arthritis, as well as and other syndromes and diseases related to the levels of ARMT, Tie-2, incertin subunit alpha-1 per all and other syndromes and other syndromes and elected to treat cancer and other levels of ARMD, Tieintegrin subunit alpha-6, or integrin subunit beta-3.

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Sequence 17 BP; 5 A; 1 C; 1 G; 10 U; 0 other;
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Gaps
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y Match 1.1%; Score 13.4; DB 1; Length 17; Local Similarity 33.3%; Pred. No. 3.3e+02; hes 5; Conservative 9; Mismatches 1; Indels
                                                                                    1524 ATATTTTAACTTTA 1538
        Query Match
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AAA21376 standard; RNA; 17 BP
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1 AUAUUUUUUACUUUA 15
                                RESULT 271
                                        AAA21376
      a
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(first entry) 19-JUN-2000

AAA21376;

The present invention describes enzymatic nucleic acid molecules with RA cleaving activity, which specifically cleave RNA encoded by an aryl Nadrocearbon nuclear transporter (ARNY) gene, an integrin submuit beta 3 gene, an integrin submuit beta 3 gene, an integrin submuit beta 3 corresponding to AAA17561 and AAA1762 represent ribozyme sequences for AAA19155 to AAA19155 to AAA191522 represent this corresponding target sequences; AAA19152 to AAA19155 and AAA19155 to AAA19155 and AAA19155 to AAA19155 and AAA19155 to AAA19155 to AAA19155 to AAA19155 to AAA19155 to AAA19155 and AAA19155 to AAA2168 to AAA2161 and AAA22476 to AAA2342 represent their corresponding target sequences. C to integrin submit beta 3, and AAA22476 to AAA23262, AAA2333 to the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, integrin submit beta-3, integrin submit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARND), inflamation, and arthritis, as well as madoche to treat cancer, diabetic retinopathy, age related and diseases related to the levels of ARNT, Tie-2, and diseases related to the levels of ARNT, Tie-2, and disease related to the levels of ARNT, Tie-2, and disease related to the levels of ARNT, Tie-2, and disease related to the levels of ARNT, Tie-2, and disease related to the levels of ARNT, Tie-2, and disease related to the levels of ARNT, Tie-2, and di ö Human; aryl hydrocarbon nuclear transport; ARNT; TIB-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; harmerhead ribozyme; angiogenic factor; cytostatic; antidabetic; ophthalmologic; antinflammatory; antiarthritic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; poriasis; verruca vulgaris; angiofibroma; tuberous sclerosis; pot-whne stain; Sturge Weber syndrome; Rippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss. Gaps Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors ÷ Jarvis T, Coeshott C, McSwiggen JA; Length 17; Indels integrin subunit alpha-6, or integrin subunit beta-3. 1.1%; Score 13.4; DB 1; 46.7%; Pred. No. 3.3e+02; tive 7; Mismatches 1; Sequence 17 BP; 6 A; 1 C; 1 G; 9 U; 0 other; Claim 55; Page 204; 305pp; English. 1617 AAAATATAATTTGTT 1631 99WO-US06507. (RIBO-) RIBOZYME PHARM INC. Query Match
Best Local Similarity 46.7%
Matches 7; Conservative Pavco PA, Roberts E, WPI; 1999-591315/50. Homo sapiens. W09950403-A2 24-MAR-1999; 27-MAR-1998; 07-OCT-1999. ठ

AAA22695 standard; RNA; 17 BP. 2 AAAAUAUAUUUUGUU 16 RESULT 272 AAA22695 ID AAA2 셤

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Human, aryl hydrocarbon nuclear transport, ARNT, TIE-2; angiogenesis, integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verucar vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Rippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an anglogenic factors
                                                                                                                                                                                                                                                                                                                                                                                     Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.1%; Score 13.4; DB 1; Length 17; Best Local Similarity 26.7%; Pred. No. 3.38+02; Matches 4; Conservative 10; Mismatches 1; Indels
                                                               Integrin subunit beta 3 substrate sequence SEQ ID NO:5921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 5 A; 0 C; 0 G; 12 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 54; Page 236; 305pp; English.
                                                                                                                                                                                                                                                                                                                                  98US-0079678.
                                                                                                                                                                                                                                                                                                       99WO-US06507,
                                                                                                                                                                                                                                                                                                                                                        (RIBO-) RIBOZYME PHARM INC.
                                      19-JUN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                       24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                27-MAR-1998;
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The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl Nydrocarbon muclear transporter (ARNY) gene, an integrin subunit beta 3 gene, an integrin subunit peets 3 gene, an integrin alpha 6 subunit gene, or Tie-2 gene. AAA16775 to AAA17165 and AAA1768 to AAA1768 to AAA196775 to AAA19155 to AAA191560 and AAA17685 to AAA19185 and AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA19185 to AAA19187 to AAA19185 to AAA19182 represent their corresponding target sequences; AAA19185 to AAA21889 to AAA21889 to AAA2189 represent their corresponding target sequences; AAA21689 to AAA2188 represent their corresponding target sequences; AAA21689 to AAA2188 represent their corresponding target sequences for integrin subunit beta 3, and AAA22476 to AAA23342 to AAA23343 to Ct and AAA2189 to AAA22263 to AAA23342 to AAA23343 to Ct and AAA2189 to AAA23283 to AAA23342 represent their corresponding target sequences for integrin subunit beta 3, and AAA22476 to AAA23362, AAA23343 to the invention are used for modulating the sequences. The ribozymes of the invention are used for modulating the subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as corresponding angiofibrome of tuberous sclerosis, potwine stains, sturge Weber corresponding the syndrome, sippel-Trenaumay-Weber syndrome, osler-Weber-Rendu syndrome, there syndromes end diseases related to the levels of ARMT, Tie-2, theories and other syndrome, when the syndrome, when the syndrome of the tender cancer in them the levels of ARMT, Tie-2, theorem.
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Gaps

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Length 17; 1; Indels

The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor. BAR3/COUP-TR-1, the GATA transcription factor gene, IRP-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha.

Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin -

Claim 37; Page 63; 164pp; English.

Blatt L, Zwick M, Pavco P, McSwiggen J;

WPI; 2000-647423/62.

L1-APR-2000; 2000WO-US09721.

99US-0129390

L2-APR-1999;

(RIBO-) RIBOZYME PHARM INC.

Ribozyme; erythropoietin; granulocyte colony stimulating factor;

interferon alpha; ss.

WO200061729-A2.

19-0CT-2000.

Homo sapiens.

Hammerhead ribozyme substrate #349.

(first entry)

16-FEB-2001

AAF02054;

AAF02054 standard; DNA; 17 BP.

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Query Match
1.1%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 3.38+02;
Matches 14; Conservative 0; Mismatches 1;
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AAF02054/c

ID AAF02054/c

AAF02

XX AAF02

XX AAF02

XX AAF02

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libozyme; erythropoletin; granulocyte colony stimulating factor;
                                                                                                 Hammerhead ribozyme substrate #2465.
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15 AAAATAAATTATTT 1
                                               AAF04949 standard; DNA; 17
                                                                                (first entry)
                                                                                                                            interferon alpha; ss.
                                                                                                                                                           WO200061729-A2
                                                                                                                                            Homo sapiens.
                                                                                 16-FEB-2001
                                                                AAF04949;
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19-OCT-2000
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Matches
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                                                                                                                                                                                                                                                                                             The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TP-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of exythropoietin, granulocyte colony stimulating factor protein and interferon alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                   Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 3.3e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17 BP; 7 A; 1 C; 2 G; 7 T; 0 other;
                                                                                                                                       McSwiggen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McSwiggen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hammerhead ribozyme substrate #2744.
                                                                                                                                                                                                                                                                  Claim 4; Page 112; 164pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blatt L, Zwick M, Pavco P,
                                                                                                                                     Blatt L, Zwick M, Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-APR-2000; 2000WO-US09721
                                                                          99US-0129390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0129390
                                                                                                        (RIBO-) RIBOZYME PHARM INC.
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Best Local Similarity 93.3
Matches 14, Conservative
                                                                                                                                                                     WPI; 2000-647423/62.
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                                                                          12-APR-1999;
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Claim 18; Page 118; 164pp; English

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The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor. BAR3/COUP-FP. 1, the GATA transcription factor gene, IRR-2 and/or the CAAT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, gene therapy, tumour suppressor, HTPL, chromosome 10p12.1; human teetis expressed Patched like protein, testis; adrenal, liver; human teetis expressed Patche bone marrow, brain; kidney, lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL -
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                                                                                                                                                                                                                     1.1%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 3.3e+02; vative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human HTPL scanning oligonucleotide SEQ ID 1670.
                                                                                                                                                                                 Sequence 17 BP; 7 A; 1 C; 1 G; 8 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 93.3 les 14; Conservative
                                                                                                                                                                                                                         Query Match
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mapped to human chromosome 10pl2.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in thesapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potential therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis syressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    th 1.1%; Score 13.4; DB 1; Length 17; Similarity 93.3%; Pred. No. 3.38+02; 14; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 3 A; 1 C; 1 G; 12 T; 0 other;
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2001WO-US00667.
2001WO-US00668.
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2001US-0864761.
2001US-0327898.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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30-JAN-2001;
30-JAN-2001;
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09-OCT-2001;
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Matches
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XX ABV8
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shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10p12.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (IRG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous selevosis; port-wine stain; wound healing; sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotide which down regulates expression of Ets-related gene, useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                             1.1%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 3.3e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 4 A; 2 C; 1 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 63; 149pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 TATABABATAGCABA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK17631 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 93.3
es 14; Conservative
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cc vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge veber syndrome, Kippel-Trenaumay-Reber syndrome, Osle-Weber-rendu comparise, Rippel-Trenaumay-Reber syndrome, Osle-Weber-rendu comparise, Sturge syndrome, Leukaemia, osteoporosis and wound healing. [I] is useful for treating a patient having a condition associated with the level of ERG, comparating cells of the patient with (I) under conditions suitable for the treatment. Leukaemia or tumour comparises the use of one or core therapies comparating comparises the use of one or core therapies complunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or cell, by contacting (I) is useful for reducing ERG activity in a coll of seasos related to the expression of ERG, and as diagnostic tool to diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically cargeting genes that share homology with ERG gene or ERG funding antisense and ABKI7354-ABKI2719 represent nucleic acids, including antisense and centared PCR primers of the invention.
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Sequence 17 BP; 8 A; 2 C; 1 G; 6 U; 0 other;

ő ö Length 17; 1; Indels 1.1%; Score 13.4; DB 1; 93.3%; Pred. No. 3.3e+02; ive 0; Mismatches 1; Local Similarity 93.3%; se 14; Conservative Query Match Best Loca Matches

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7632/c ABK17632 standard; RNA; 17 BP. RESULT 279 ABK17632/c

ABK17632;

09-APR-2002 (first entry)

Human ERG hammerhead ribozyme target sequence, Seq ID No 279.

Human, hammerhead ribozyme, cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphome; Ewing's sarcoma; melanoam; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; vertuca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay;Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme; amberzyme.

Homo sapiens.

WO200188124-A2.

22-NOV-2001.

16-MAY-2001; 2001WO-US15866.

L6-MAY-2000; 2000US-0572021

(RIBO-) RIBOZYME PHARM INC. (GLAX) GLAXO GROUP LTD.

Jarvis T,

WPI; 2002-082995/11.

Von Carlowitz I, McSwiggen JA, Mclaughlin F, Randi AM;

Novel polynucleotide which down regulates expression of Ets-related gene, useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber

Claim 4; Page 63; 149pp; English.

The invention relates to a nucleic acid colecule (I) which down regulates corpression of an Ebe-related gene (ERG). (I) is useful for treating.

Conditions selected from cancer, lymphoma, Bwing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, conditions angiofibroma, myopic degeneration, arthritis, psoriasis, verruca vulgaris, angiofibroma, of tuberous sclerosis, port-wine stains, Sturge Weber syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting calls of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies to the treatment. The method comprises the use of one or more therapies or under conditions suitable for the treatment is eukaemia or tumour conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or call, by contacting (I) is useful for reducing ERG activity in a cell, by contacting (I) with RNA, in the presence of advalent coll to diseases related to the expression of RRG, and as diagnostic coll to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically creating genes that share homology with RRG gene or ERG fusion genes. ABRIJ354-ABRIZ279 represent nucleic acide molecules which regulate expression of ERG, and created PCR primers of the invention.

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Sequence 17 BP; 7 A; 2 C; 2 G; 6 U; 0 other;

Gaps .. 1.1%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 3.3e+02; ive 0; Mismatches 1; Indels Local Similarity 93.3 nes 14; Conservative Query Match Matches

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ઢ 셤 RESULT 280 ABA02551

ABA02551 standard; DNA; 17 BP. ABA02551;

26-MAR-2002 (first entry)

Human ADAMTS-M PCR primer (reverse).

Osteoarthritis, rheumatoid arthritis; inflammatory bowel disease; Crohn's disease; asthma; Alzheimer's disease; organ transplant rejection; cachexia; allegy; cancer; leukaemia; lymphoma; osteoporosis; atherosclerosis; congestive heart failure; myocardial infarction; stroke; neurodegenerative disease; autoimmune disorder; Huntingfon's; parkinson's migraine; pain, depression; multiple sclerosis; burn; infertility; diabetic shock; gene therapy; ADAMTS-M; PCR; primer; ss; A Disintegrin And Metalloprotease; thrombospondin domain;

Homo sapiena.

BP1152055-A1.

07-NOV-2001.

24-APR-2001; 2001BP-0303706.

2000US-200040P 27-APR-2000;

(PFIZ) PFIZER PROD INC.

Walsh RT; Wachtmann TS, Suckbinder L, Mitchell PG, Tuljnder M;

Amson R,

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ABT34735;
                   Query Match
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(MOLE-) MOLECULAR ENGINES LAB.
                                                                                                                                             WPI; 2003-313353/30
   The present sequence represents a PCR primer used to screen a panel of CDNA libraries to determine a source for further cloning of novel CDNA libraries to determine a source for further cloning of novel CDNA libraries to determine a source for further cloning of novel CDNA libraries to determine a thrombospood in ABA02549) that cancedes the ADAM (A Disintegrin And Metalloprotease) family of metalloproteases, and contains a thrombospondin domain (TS). The specification describes a newly isolated polymuclectide, comprising a mucleotide sequence encoding an ADAMTS-M polypeptide as given in the specification, or a metalloproteinase, disintegrin domain, prodomain or its thrombospondin submotif. The polymuclectide, polypeptide and agent care useful for manufacturing a medicament for treating activity or expression of ADAMTS-M. The polymuclectide, and agent or are useful for manufacturing and agent are useful for manufacturing a medicament of a ltering activity or expression of ADAMTS-M. The polymuclectide, not a medicament of a ltering activity or expression of ADAMTS-M. The polymuclectide, organ transplant toxicity and rejection, cachesia, allergy, cancer (e.g. cogan transplant toxicity and rejection, cachesia, allergy, cancer (e.g. coing tumour cancer including colon, breast, lung, prostate, brain or haematopoietic malignancies including leukaemia and lymphoma), corpusorosis, atherosolerosis, aortic aneurysm, congestive heart failure, meurodegenerative disease, autoimmune disorders, Huntington's disease, abnormal wound healing, burns, infertility or diabectic shock. The polymuclectide and polypeptide are also useful for diagnosing the polymuclectide and polypeptide are also useful for diagnosing the construction when the since a lago useful for diagnosing the construction when the since a lago useful subsection in the polymosories and the polymosories and polymosor
                                                                                                        New polynucleotide, useful in gene therapy, particularly for treating or preventing e.g. arthritis, Crohn's disease, Alzheimer's disease and organ transplant toxicity and rejection, comprises ADAMTS polynucleotide and encoded polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases above. The polynucleotide is for treating the diseases cited above.
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                                            WPI; 2002-084275/12.
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Query Match
                             Matches
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                                                          Gaps
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                          1.1%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 3.3e+02; rative 0; Mismatches 1; Indels
Sequence 17 BP; 6 A; 6 C; 2 G; 3 T; 0 other;
                                          Local Similarity 93.3
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Tumour suppression related human fukutin oligo SEQ ID No 372.
                                                                                                                                                                           ABT34735 standard; DNA; 17 BP
754 TGTGATATTTGAAGC 768
                             15 TGTGATATTTGGAGC 1
                                                                                                                                                                                                                                                                                12-JUN-2003 (first entry)
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Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds.

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17-SEP-2002; 2002WO-IB04208.
                                                                                                                                                17-SEP-2001; 2001FR-0011978.
                                  WO2003025175-A2
Homo sapiens
                                                                       27-MAR-2003.
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(MOLE-) MOLECULAR ENGINES LAB

17-SEP-2001; 2001FR-0011978. 17-SEP-2002; 2002WO-IB04208.

WO2003025175-A2. Homo sapiens

27-MAR-2003.

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consecutive nucleotides from the 17 mer sequence, a sequence with, after consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti) sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, collapsed that are characterised by development of tumours or cell preparation, specificalls for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and attent samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequence represents a tumour suppression characterial human fukutin oligonucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds.
                                                                                                                                                                            The invention relates to a novel isolated 17 mer nucleic acid sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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New isolated mucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour suppression related human fukutin oligo SEQ ID No 675.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 8 A; 3 C; 3 G; 3 T; 0 other;
                                                                                                                       Disclosure; Page 77; 720pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               534 TCAGTAAACAATGAA 548
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les 14; Conservative
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Thu Dec 18 07:29:20 2003
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The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after contecutive nucleotides from the 17 mer sequence, a sequence with, after contecutive nucleotides from the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagants, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the polypeptides are useful for preparation of pharmaceuticials for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell desentation, specifically cancer but also Alzheimer's disease and schints analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and chops. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression related human fukutin oligonuclectide of the invention. New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells -Disclosure, Page 113; 720pp; French Telerman A, Amson R, Tuijnder M; WPI; 2003-313353/30.

Sequence 17 BP; 9 A; 1 C; 3 G; 4 T; 0 other;

Gaps ö Query Match
1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels

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ABT39610;

ABT39610 standard; DNA; 17 BP

Tumour suppression related human fukutin oligo SEQ ID No 5247.

12-JUN-2003 (first entry)

Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds. RESULT 283
ABT39610
XX
AC ABT396.
AC ABT396.
DT 12-JUN
XX
DX CYtOST
XW antise
XW antise
XW antise
XW ACOURT
XW ACOUR

Homo sapiens

WO2003025175-A2.

27-MAR-2003.

17-SEP-2002; 2002WO-IB04208

(MOLE-) MOLECULAR ENGINES LAB 17-SEP-2001; 2001FR-0011978

Tuijnder M; relerman A, Amson R,

WPI; 2003-313353/30.

schultz143-3.rng

New isolated mucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells

Disclosure, Page 647; 720pp; French

The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence, a sequence that uncleotides from the 17 mer sequence, a sequence that nybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding NNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, and for production of recombinant polypeptides. Any of the nucleic acids, onlypeptides, vectors containing the nucleic acids, colls containing the nucleic acids, cells containing the nucleic acids, cells containing the nucleic acids, cells containing the nucleic acids of preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell diseases that an characterised by development of tumours or cell diseases the polypeptides can also be used to generate antibodies, and patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and chips. The nucleic acid sequences of the invention can be used in gene therapy. This polymucleotide sequence represents a tumour suppression crelated human fukutin oligonucleotide of the invention.

Sequence 17 BP; 6 A; 1 C; 2 G; 8 T; 0 other;

Gaps 0; Match 1.1%; Score 13.4; DB 1; Length 17; Local Similarity 93.3%; Pred. No. 3.3e+02; es 14; Conservative 0; Mismatches 1; Indels Query Match Matches

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RESULT 284

ABZ61156 standard; RNA; 17 BP

AB261156;

Human K-Ras DNAzyme substrate #1268. 21-MAR-2003 (first entry)

Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras; enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV; anti-rheumatic; cancer; AIDS; ss.

Homo sapiens.

WO200297114-A2.

05-DEC-2002.

29-MAY-2002; 2002WO-US16840

29-MAY-2001; 2001US-294140P. 06-UUN-2001; 2001US-296249P. 10-SEP-2001; 2001US-318471P.

(RIBO-) RIBOZYME PHARM INC

Mcswiggen J;

WPI; 2003-140484/13

888888888

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Gaps

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1; Indels

Query Match 1.1%; Score 13.4; DB 1; Length Best Local Similarity 93.3%; Pred. No. 3.3e+02; Matches 14; Conservative 0; Mismatches 1; Indels

1332 TCCCAGTCTTGTCAT 1346

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15

14; Conservative

AAA63708 standard; DNA; 18 BP

RESULT 286 AAA63708

Sequence 17 BP; 7 A; 2 C; 7 G; 1 U; 0 other;

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Novel short interfering RNA and enzymatic nucleic acid useful for treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences
                                                                                                                                                                                                                                                        Claim 58; Page 132; 185pp; English.
                                                                                                                                                                                                                                  WPI; 2003-140484/13.
                                                                                                                 Matches
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                                                                                                                                                                                             The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytostatic, anti-HIV, and reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The mucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABESSB89 - ABESGESIG, ABESGESIG, ABESGESIG, ABESGESIG, RESESSII, sequences for the human ribozymes of the invention.
Novel short interfering RNR and enzymatic nucleic acid useful for treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gape
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enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
anti-rheumatic; cancer; AIDS; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.1%; Score 13.4; DB 1; Length 17; 26.7%; Pred. No. 3.3e+02; ative 10; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17 BP; 4 A; 2 C; 0 G; 11 U; 0 other;
                                                                                                                                          Claim 58; Page 109; 185pp; English.
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06-JUN-2001; 2001US-296249P.
10-SEP-2001; 2001US-318471P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABZ62202 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 26.7 es 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-DEC-2002
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PCR primer used to amplify a fragment of the FRI locus.

(first entry)

04-DEC-2000

AAA63708;

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                                                                                                                   H51; one locus-FRIGIDA; FRI gene; flowering time; blotting;
flower initiation; stem elongation; flower production; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid derived from the FRI locus of a plant, e.g. Arabidopsis, encoding a polypeptide capable of specifically altering the flowering time of a plant -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.1%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 3.5e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 BP; 3 A; 4 C; 3 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   flower production across the seasons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 43; 73pp; English.
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                                                                                                                                                                                                                                                                                                                                         (PLAN-) PLANT BIOSCIENCE LTD
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Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-532899/48.
                                                                                                                                                                                                      WO200046358-A2.
                                                                                                                                                                   Arabidopsis sp.
                                                                                                                                                                                                                                                                                                         05-FEB-1999;
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The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic

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Wild type sequence for ABC1 polymorphic site #28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense compound which modulates human sentrin expression, useful for treating diseases associated with sentrin expression -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an antisense compound (I) 8-30 nucleotides long targeted to a nucleic acid molecule encoding human sentrin. The antisense compound comprises a phosphorothicate antisense oligonucleotide which inhibits expression of human sentrin. (I) is useful for inhibiting expression of sentrin in human cells or tissues in vitro, for treating humans or other animals suspected of having or being prome to a disease associated with sentrin expression. (I) can also be used for research or diagnostic purposes. The present
                                                                                                                                                                                                                                                     Human sentrin phosphorothioate antisense oligonucleotide SEQ ID NO:31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence represents a human sentrin phosphorothioate antisense oligonuclectide from the present invention.
                                                                                                                                                                                                                                                                                          Human, sentrin, antisense oligonuclectide; phosphorothioate, inhibition, modulation; expression; diagnosis; ss.
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/note= "phosphorothioate linkages"
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                                                                                                                              AAZ35889 standard; DNA; 18
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TTTGATGTGCTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 93.3
Matches 14; Conservative
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modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-DEC-1998;
                                                                                                                                                                                                             03-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                      AAZ35889;
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AAF92967
ID AAF9299
XX
AC AAF9291
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DT 17-MAY
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AAZ35889
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High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or ardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABC1 expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition sele lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                feast, platelet activating factor acetylhydrolase, PAF-AH; 8s;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.1%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 3.5e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 BP; 10 A; 1 C; 5 G; 2 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                705 AAGAGAATATCCGAA 719
                                                                                                                                                                                                                                                                                                            01-SEP-2000; 2000WO-IB01492.
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23-JUN-2000; 2000US-0213958.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (XENO-) XENON GENETICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for preventing diabetes mellitus comprising administering a platelet activating factor acetylhydrolase (PAF-AH) product to a subject at risk of developing diabetes mellitus. The method is also used to slow the progression of diabetes mellitus in a patient suffering from the disease. This sequence represents a Saccharomyces cerevisiae PAF-AH DNA related oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                 Preventing diabetes mellitus comprises administering a platelet activating factor acetylhydrolase product to a subject at risk of developing the disease -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.1%; Score 13.4; DB 1; Length 18; 93.3%; Pred. No. 3.5e+02; lve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer #2 to amplify repeat sequence marker Mfd108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 BP; 4 A; 1 C; 4 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Column 13-14; 186pp; English
                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 14; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1282 ATTATTGTTTATCTG 1296
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89US-0341562.
94US-0222177.
                            99US-0306970.
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(first entry)
                                                                                                                                 Peterman GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 93.3
Matches 14, Conservative
                                                                                                                                                                                    WPI; 2002-673986/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-042299/04.
                                                                            (ICOS-) ICOS CORP.
                            07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-1989;
04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
18-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5582979-A
                                                                                                                                 Dietsch GN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weber JL;
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The invention relates to the isolation of polymorphic repeat sequences

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having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The primers AAT65098-T66047 were used to PCR amplify the inserts from the isolated clones containing the repeat sequences. The primers AAT66012-3 were used to amplify the repeat sequence marker clone Midlo8 (AAT65779).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAX02153-X02161 are primers used in a method for detecting one or more base-pair mutations in a nucleic acid sequence by differentiating heteroduplexes from homoduplexes. The method involves generating homoduplexes and heteroduplexes in a sample and performing gel electrophoresis on the sample using a polyacrylamide gel that causes heteroduplexes to migrate more slowly than homoduplexes. The gel comprises 3-20% polyacrylamide, 1-50% of at least one denaturing eslected from alibhatic alcohols, cyclic alcohols, alicyclic compounds, amides, ureas and carbamates, 10-100 mM borate-free TB [Tris-HCl, BDTA] buffer, and 10-100 mM taurine. The method has a high reliability and can be improved by allowing for the presence of the mutations in domains with high melting temperatures. These primers can specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVS17 acceptor splice site; PCR primer; detection; base-pair mutation; heteroduplex; homoduplex; migration; ss.
                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of nucleic acid mutations - by electrophoresis in polyacrylamide gel that distinguishes heteroduplexes from
                                                                                                                                                                                                                                                                                                                                  Length 19;
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human IVS17 3'-acceptor splice site PCR primer #8.
                                                                                                                                                                                                                                                                                                                              1.1%; Score 13.4; DB 1;
93.3%; Pred. No. 3.6e+02;
ative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                       Sequence 19 BP; 4 A; 10 C; 1 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Column 5; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rock MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYJE-) UNIV JEPPERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                     957 AGTGATGTTGTGAGG 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0468551.
93US-0061574.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 Agreardrefreezase 3
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                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-179967/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homoduplexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5874212-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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                                                                                                                                                                                                                                                                                                                                    Query Match
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TTTTACTGTTTCTCA 15

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Ribozyme, hairpin, hammerhead, gene therapy, vasotropic;
                                                                                                                                                                                              Cyclin C ribozyme binding site #205.
            1567 TITTACTGTTTCTGA 1581
                                                                                                         AAA84233 standard; DNA; 19 BP
                                                                                                                                                                 04-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            (IMMU-) IMMUSOL INC.
                                                                                                                                                                                                                                        restenosis; ss.
                                                                                                                                                                                                                                                                                              WO200032765-A2
                                                                                                                                                                                                                                                                                                                                                      06-DEC-1999;
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                                                                                                                                       AAA84233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention, which contain a polymorphic base at position 24 of their nuclectide sequences. AAZ69579 to AAZ71440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ65654 to AAZ69578 represent human biallelic markers from the present
                                                                                 Gaps
                                                                                                                                                                                                                                                                                              Human biallelic marker upstream amplification primer SEQ ID NO:4969.
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                                                                                                                                                                                                                                                                                                                      Human genome, biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymczphic base; gentotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
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detect a mutation in the human IVS17 3'-acceptor splice site.
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                                                      Length 19;
                                                                                 1; Indels
                                                    Query Match
1.1%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 2 A; 5 C; 2 G; 10 T; 0 other;
                           Sequence 19 BP; 8 A; 3 C; 6 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chumakov I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Page 1290; 2745pp; English.
                                                                                                                                                                                                             AAZ70613 standard; DNA; 19 BP.
                                                                                                              B18 GCTGGAAATCCTGGA 832
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                                                                                                                                       1 Geregaaaacereca 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       map of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-013267/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                   diagnosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                         W09954500-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-APR-1998;
23-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment
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99WO-US28772. 98US-0110954.

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                                                                                                                                                                                                                                          The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CNZI, PCNA and Cyclin Bl. Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment.
                                                                                           New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat; expression profile; Three Prime End Amplification; TPRA; adenosine receptor 2a; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 19; Score 13.4; DB 1; Length 19; Local Similarity 93.3%; Pred. No. 3.6e+02; les 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat adenosine receptor 2a forward PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 8 A; 3 C; 4 G; 4 T; 0 other;
Robbins JM
                                                                                                                                                                                                  Disclosure; Page 74; 109pp; English.
Barber JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ89251 standard; DNA; 19 BP
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Tritz R, Welch PJ,
                                                WPI; 2000-412314/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ89251;
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Matches
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Gaps

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AAH90994;

05-AUG-1999; 05-AUG-1998;

17-FEB-2000

Rattus sp.

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The present invention describes a method for detecting the presence of polymorphisms associated with inflammatory bowel diseases such as udcerative collitis and Crohn's disease. The methods can be used to detect the presence of genetic polymorphisms associated with inflammatory bowel disease and correlating their occurrence with disease states. They may be used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a polymorphic site described in the exemplification of the invention.
                                                                                                                                                                Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis; single nucleotide polymorphism; SNP; chromosome 19p13; paternity test; chromosome 5q31-33; forensic test; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Testing for the presence of polymorphisms associated with inflammatory bowel disease, using a hybridization assay -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense oligonucleotide, groß, großi, groß; inhibitor; growth; microorganism; Bscherichia coli; Streptcococus pneumoniae; diagnosis; Streptcococus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa; antibacterial; antiviral; antiproliferative; antisense therapy;
                                                                                                                Human inflammatory bowel disease associated polymorphic site #69.
                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "SNP, optionally A or T at this position"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S. aureus groß operon antisense oligonucleotide SEQ ID NO:406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.1%; Score 13.4; DB 1; Length 19; 87.5%; Pred. No. 3.6e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lander BS, Rioux J, Siminovitch K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19 BP; 5 A; 0 C; 1 G; 12 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BLLI-) RILIPSIS BIOTHERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (WHED ) WHITEHEAD INST BIOMEDICAL RES
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 42; 463pp; English.
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                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saly M, Hudson TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200142511-A2
                                                                        09-OCT-2001
                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                    misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH56758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH56758,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel process (M1) of reverse transcribing mRNA species present in a sample from an organism by: (a) reverse mRNA species present in a sample from an organism by: (a) reverse cranscribing the mRNA species using a first heeled primer, to provide a first strand cDNA species and (b) synthesizing second cDNA species of the card inside a second heeled primer population, the nucleotide sequences of the non-heel portions of the second heeled primers being such that the crow-rese transcribed first strand cDNA species can be used for expression conformance and a heel sequence 5' can be used for the reverse transcription of mRNA species in a sample. The polynucleotide primer oppulation of claim (4) can be used for the synthesis of second strand cDNA species. Single cell cDNA.

Conformation a population of first strand cDNA species. Single cell cDNA.

Conformation of claim (4) can be used for the synthesis of second strand cDNA species. Single cell cDNA.

Conformation of claim (4) can be used for the synthesis of second strand cDNA species. Single cell cDNA.

Conformation of claim (4) can be used for the synthesis of second allow and the discovery of novel genes. Small samples can be used available for complex issues. The invention provides a rapid, robust and reproducible can the using can be used for the analysis of gene expression the complex issues. The invention provides are limiting. Whilst in situ hybridization technique sprovide detailed information about the complex insues provide synthin asingle cells or small tissue samplists are limiting. An expression pattern of a gene in intact tissue the technique is can intact in a single to separation. The methods for the analysis of gene expression cellular expression pattern of a gene in intact tissue the technique of preparation. The methods presented in the disclosure provide a more consulting that even relatively low abundance mRNA species are transcribed in the analyzed. There is a bias covards more uniform the primers described in the abu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                    Reverse transcription of mRNA species used for expression profiling of single cells by employing a first heeled primer to provide first strand CDNA species and then a second heeled primer population to generate second strand cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 3.6e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 6 A; 6 C; 4 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                              Freeman TC, Richardson PJ, Dixon AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 30; 50pp; English.
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AAH90994
ID AAH90994 standard; DNA; 19 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1348 GCCAGCTGTGTTGGT 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.18;
                                                                                                                                                                              99WO-GB02579.
                                                                                                                                                                                                                           98GB-0017055
                                                                                                                                                                                                                                                                              (MEDI-) MEDICAL RES COUNCIL.
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                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-224033/19.
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                                                                        WO200008208-A2
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Gaps

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Query Match Best Local Matches

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(GENE-) GENESENSE TECHNOLOGIES INC.
                                                                                                                                                                                              99US-0166249.
                                                                                                                                                      20-NOV-2000; 2000WO-CA01347
microbial infection; ss
                                     Staphylococcus aureus.
                                                                             WO200136625-A2
                                                                                                                                                                                              18-NOV-1999;
                                                                                                                  25-MAY-2001
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Wright JA, Young AH, Dugourd D;

WPI; 2001-355633/37.

Novel antisense compounds targeting nucleic acid encoding groEL or groES gene of microorganism, which hybridize with and inhibit expression of the genes, useful to inhibit growth of microorganism having the genes -

Claim 3; Page 52; 110pp; English.

The present invention specifically claims AAH56368 to AAH56812 which are antisense oligonucleotides to nucleotide sequences encoding groE. More generally, antisense compounds (1) comprising antisense oligonucleotides of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a nicroorganism, where the antisense compound is complementary to GL or GS of a nicroorganism and specifically hybridises with and inhibits the antiprolliferative activities, and can be used in antisense therapy and for inhibition of expression of GL or GS in cells or tissues in vitro. (I) are antiprolliferative activities, and can be used in antisense therapy and for inhibition of expression of GL or GS in cells or tissues in vitro. (I) are also useful for inhibiting the growth of a microorganism, or inhibiting the growth of a microorganism, or inhibiting the growth of anticoorganism, or inhibiting the growth of anticoorganism or to a cell infected with the microorganism of to a cell infected with the microorganism pathological condition mediated by microorganism pathological condition mediated by microorganisms which involves identifying a eukaryotic organism by the midroorganisms which involves identifying a condition mediated by the provent or delay microbial infected with the microorganisms having a gloof condition mediated by microorganisms which involves identifying a cloor or declay microbial infected with the growth of microorganism is inhibited. The antiense compounds are utilised for diagnostics, the microorganism ship involves in humans. They are also useful as molecular weight markers. AME6362 to AME66357 and AME68370 represent exemplification of the present invention. AME68870 represent

Sequence 19 BP; 6 A; 1 C; 0 G; 12 T; 0 other;

Gaps ö Match 1.1%; Score 13.4; DB 1; Length 19; Local Similarity 93.3%; Pred. No. 3.6e+02; Losservative 0; Mismatches 1; Indels Query Match Matches

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AAH59395 Btandard; DNA; 19 AAH59395;

(first entry) 10-SEP-2001 Cyclin C ribozyme binding site SEQ ID NO:1819.

Human, ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnerary; proliferative disease; skin disease; gotistasis; diabetic: retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MWP; matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; antiseoriatic; dermatological; antiseborrheic; antidiabetic; vincide; antisickling; ophthalmological; keratolytic; gene therapy; viral wart; atopic dermatitis; actinic keratosis; squamous cell carcinoma; basal cell carcinoma; heborrheic wart; vitreoretinopathy; scar; sickle cell retinopathy; ss

sapiens 000

Synthetic.

WO200130362-A2.

03-MAY-2001.

26-OCT-2000; 2000WO-US29500.

26-OCT-1999, 99US-0161532

(IMMU-) IMMUSOL INC.

Robbins JM, Tritz R;

WPI; 2001-300427/31

Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases -

Example 1; Page 204; 408pp; English.

The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (I) which cleaves RNA encoding a cytckine involved in inflammation, matrix metalloproteinase (WMP). cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (I). (I) can have antipsoriatic, dermatological, cytostatic, antisebortheic, antidiabetic, antisickling, obthalmological, vulnerary, keratolytic and virucide activities, and cleaves RNA encoding cytchine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing prematuring such as keloid, adhesion and hypertrophic or hypertrophic burn scar. AMESTST7 to AMH62099 represent sequences used in the exemplification of the present invention.

Sequence 19 BP; 8 A; 3 C; 4 G; 4 T; 0 other;

Gaps .. 1.1%; Score 13.4; DB 1; Length 19; 13.3%; Pred. No. 3.6e+02; ve 0; Mismatches 1; Indels 93.3%; Ouery Match Best Local Similarity 93.39 Marches 14; Conservative

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AAF57945 standard; DNA; 19 AAF57945; RESULT 298 AAF57945/C ID AAF5794 ង្គង្គ

BP

20-APR-2001 (first entry)

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Nucleic acid amplification; low abundance sequence; expression profiling; high throughput analysis; PCR primer; ss.
                                                                                                                                                                                                                               Increasing the number of nucleotide sequences for low quantity mRNA species from a sample for detection and cloning of gene sequences -
       Low abundance nucleic acid amplification PCR primer #16.
                                                                                                                                                                   (UYCA-) UNIV CAMBRIDGE TECH SERVICES.
                                                                                                                                                                                                                                                               Example 1; Page 110; 120pp; English.
                                                                                                                         19-JUL-2000; 2000WO-EP06887.
                                                                                                                                              99US-0144666
                                                                                                                                                                                       Richardson P, Cox P;
                                                                                                                                                                                                           WPI; 2001-138470/14.
                                                                                 WO200106004-A2
                                                                                                                                              19-JUL-1999;
                                                                                                     25-JAN-2001
                                                            Synthetic.
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The present invention describes methods of increasing the number of nucleic acid sequences corresponding to an mRNA present in a sample using heeled primer sequences in amplification reactions. This is useful in the detection and cloning of low copy number mRNAs in a sample, in expression profiling and in high throughput systems.

Sequence 19 BP; 6 A; 6 C; 4 G; 3 T; 0 other;

Gaps ö Query Match 1.1%; Score 13.4; DB 1; Length 19; Best Local Similarity 93.3%; Pred. No. 3.6e+02; Matches 14; Conservative 0; Mismatches 1; Indels 1, Indels

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1348 GCCAGCTGTGTTGGT 1362 S 19 GCCAGCTTTGTTGGT

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ABS97159 standard; DNA; 19 BP. ABS97159; RESULT 299

23-DEC-2002 (first entry)

Human CYP4501A2 Exon 3 PCR primer #2.

Human; 88; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; WDR1; PCR;
Cytochrome P450 A2; CYP4501A2; cytochrome P450 02B; CYP45002E1; LTF;
Adrenorgic receptor beta1; ADBR1; aryl hydrocarbon, ARR; WRP3; NRT1Z;
Adrenorgic receptor nuclear translocator; ARNT; cathepsin S; CTSS;
Cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
Cyclooxgenase 2; COX2; diazepam binding inhibitor;
Cyclooxgenase 2; COX2; diazepam binding inhibitor;
Cyclooxgenase 2; COX2; diazepam;
Cyclooxgenase 2; COX2; nicoteans pransferase;
Cyclooxgenase 2; NQC2; ulfortansferase;
Cyclooxgenase 2; NQC2; ulfortansferase;
Cyclooxgenase 2; NQC2; ulfortansferase;
Cyclooxgenase receptor;
Cyclooxgenase 2; COX2; diazepam;
Cyclooxgenase 2; d central nervous system; pulmonary; immunological

Homo sapiens

WO200257410-A2.

25-JUL-2002.

28-NOV-2001; 2001WO-US44838

28-NOV-2000; 2000US-0724389.

(DNAS-) DNA SCI LAB INC.

Suida M, Hall J;

WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrone p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits

Example 2; Page 100; 714pp; English

This invention relates to the sequence of an isolated mucleic acid molecule comprising at least one base variation from that of a known human cytcochrome P450 Al (CYP4501A1), Cytcochrome P450 A2 (CYP4501A2), aryl bydrocarbon receptor nuclear translocator cytcochrome P450 02E1 (CYP45002E1), adrenergic receptor betal (ADBR1), aryl bydrocarbon receptor nuclear translocator (ARMY), cathepain 8 (CYS6), cytlocoxgenase 2 (CXX2), diazepam binding christing protein (FIAP), glutathione-S-transferase 12 (GYS12), cytlocoxgenase 2 (GXX2), diazepam binding cativating protein (FIAP), glutathione-S-transferase 12 (GYS12), cytlocoxgenase 2 (GXX2), diazepam binding cativating protein (FIAP), glutathione-S-transferase 12 (GYS12), unclaime-N-methyl transferase (HNMY), (Kallikrain 2) KIXZ, nicothiamide cylocarbor transferase (HNMY), MadpH quinone oxidoreductase 2 (KXX2), cylocarbor transferase (HNMY), multidung resistance associated (GYS2), or papalucuronosyl transferase 28 (GYS2N), unclained and cylocarbor transferase (HNMY), multidung resistance associated protein 3 (KRP2), orphan muclear receptor (UR12), or acetylcholine protein 3 (KRP2), orphan muclear receptor (UR12), or acetylcholine protein 3 (KRP2), orphan muclear receptor (HNI2), or acetylcholine characterising the genes that are responsible for a protein 3 (KRP2), orphan muclear transpension, constitutive expression, multiply as are useful of their early of diazorder-related traits as a result of their early of diazorder-related traits as a result of their early of diazorder-related traits as a result of their early of diazorder-related traits as a result of criat are conserved on unclaimed in CYP4501A1, CYPP4501A2, CYP4501A2, CYP4501A2, CYP4501A2, CYP4501A2, CYP4501A1, CYPP4501A2, CYP4501A1, CYPP4501A2, CYP54501A2, CYPA501A2, CYPA501A2, MULTIP, MULTIP

Sequence 19 BP; 3 A; 1 C; 8 G; 7 T; 0 other;

ö Match 1.1%; Score 13.4; DB 1; Length 19; Local Similarity 93.3%; Pred. No. 3.6e+02; les 14; Conservative 0; Mismatches 1; Indels Query Match Matches

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Gaps

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RESULT 300 AAL45792/c

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The invention relates to human CCR4 protein 10 (AAMS2938), nucleic acids encoding it (ABA02440), and a method for the recombinant production of CCR4 protein 10. The protein las a molecular weight of 10 kD. The protein last a molecular weight of 10 kD. The present invention additionally discloses an antagonist of CCR4 protein 0. for therapeutic use, and an antibody which specifically binds to CCR4 protein 10. CR4 protein 10, and nucleotides which encode it may be used for treating a variety of diseases, such as malignant tumours, blood diseases, HIV (human immunodeficiency virus) infection, immune disorders and inflammatory conditions. The protein may also be used to screen for modulators of its activity or for peptide fingerprinting identification. The polymucleotide can be used as primer for nucleic acid amplification reactions or as a probe for hybridisation reactions, or in producing gene chips or microarrays. Sequences ABA02441 raBA02442 represent reverse transcription-PCR (RT-PCR) primers used in an exemplification of the invention to isolate human CCR4 protein 10 cDNA.
                                                                                                                                                                                                                                                                                                                                                                           Human CCR4 protein 10 and encoding polynucleotide, used in diagnosis and treatment of malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-linking oligomer 702 for targetting Herpes Simplex Virus I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 73.9%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 6; Indels
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HSV; covalent cross-linking group; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= c
/mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
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/mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24 BP; 5 A; 3 C; 0 G; 16 T; 0 other;
                                                                                                                                                                          (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        673 AATATACAAATAGCAAAATTGGG 695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag= b
mod_base= OTHER
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                                 08-MAY-2001; 2001WO-CN00700.
                                                                                                       09-MAY-2000, 2000CN-0115620.
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                                                                                                                                                                                                                                                                                                                   WPI; 2002-066676/09
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modified base
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                                                                                                                                                                                                                                             Mao Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of human MGC-2413.31. The sequences can be used in the treatment of cancer, haemopathy, development disorders, HIV infection, immune disorders and inflammation. The present sequence is a PCR primer for the coding sequence of the invention.
                                                                                                                                                                                                                                                                           Human; MGC-2413.31; cancer; haemopathy; development disorder;
cytostatic; haemostatic; virucide; immunomodulatory; antiinflammatory;
immune disorder; HIV infection; inflammation; gene therapy; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide-MGC-2413.31 and encoding polynucleotide, used in diagnosis and treatment of malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; CCR4 protein 10; recombinant production; malignant tumour; cancer; blood disease; HIV infection; human immunodeficiency virus; immune disorder; inflammatory condition; gene therapy; cytostatic; anti-HIV; antiinflammatory; immunomodulator; reverse transcription-PCR; RT-PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human CCR4 protein 10 RT-PCR primer, SEQ ID NO:3.
                                                                                                                                                                                                        Human MGC-2413-31 coding sequence PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24 BP; 8 A; 2 C; 1 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1003 TAACATAAATTATTTTCAAGTGT 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 TAAAATAAATAAATTCAATGGT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 17; 34pp; Chinese.
AAL45792 standard; DNA; 24 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA02441 standard; DNA; 24 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUN-2001; 2001WO-CN01088.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000; 2000CN-0116945
                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-258028/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200220776-A1
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                                                                                                                                     28-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                      primer; ss.
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                                                                      AAL45792
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modified base

22-NOV-2001

Best Loca Matches

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Gaps

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bind to the major groove of duplex DNA and are esp. useful for
treating latent infections e.g. HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-linking oligomer 723 to target Herpes Simplex Virus I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
1.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                The oligomer is designed to target Herpes Simplex Virus I beginning at nucleotide 52916 and to covalently cross-link to it. See also AAQ20151-Q20161.
                                                                                                                                                                      /*tag= h
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                                                                                 /*tag= f
/mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
                    /note = "N-methyl-8-oxo-2'-deoxyadenine"
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/mod_base= OTHBR
/note= "N-methyl-8-oxo-2'-deoxyadenine'
                                                                                                                              /*tag= g
/mod_base= CTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 8 A; 0 C; 0 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Page 29; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1611 ACATTTAAAATATATTT 1628
/*tag= d
/mod_base= OTHER
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                               modified base
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25-MAY-1990;
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deoxyribonucleic acid; major groove; HSV; inverted polarity region; covalent cross-linking group; ss.

Location/Qualifiers 1

Key modified_base

Synthetic.

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New sequence-specific non-photo-activated crosslinking agents bind to the major groove of duplex DNA and are esp. useful for
                                                                  '*tag= c
'mod_base= OTHER
'note= "N-methyl-8-oxo-2'-deoxyadenine"
                                                                                                                                                                                                                                                                                '*tag= i
/mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
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/mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
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/mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
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/mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
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'note= "N-methyl-8-oxo-2'-deoxyadenine"
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/note= "N-methyl-8-oxo-2'-deoxyadenine"
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/mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
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|mod_base= OTHER
'note= "N-methyl-8-oxo-2'-deoxyadenine'
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'note= "N-methyl-8-oxo-2'-deoxyadenine'
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mod_base= OTHER
'note= "N-methyl-8-oxo-2'-deoxyadenine'
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"tag= 1

|abel= inverted polarity_region

"note= "see comments"
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                                                                                                                                       *tag=
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                                                                                             modified base
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25-MAY-1990;
                                                                                                                                                                                                                                                                                                             misc_feature
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'ttag= a mod_base= OTHER 'note= "N-methyl-8-oxo-2'-deoxyadenine"

/mod_base= OTHER /note= "N-methyl-8-oxo-2'-deoxyadenine"

*tag= p

modified_base

modified_base

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                                                                                                                      Gaps
                            This oligomer contains an inverted polarity region formed from an o-xyloso dimer synthon. Residues 11 and 12 are linked via an o-xyloso group (i.e. nucleotides that have xylose sugar linked via the o-xylene ring). The sequence is designed to target the Herpes Simplex virus I beginning at nucleotide 10996 and to covalently cross-link to it. See also AAQ20151-Q20161.
                                                                                                                                                                                                                                                                    Herpes simplex virus I; AIDS; modified; HIV; RSV; HFV; malignancy; hepetitis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                     /mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
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"mod_base= OTHER
"note= "OTHER= N6 methy!-8-oxo 2' deoxyadenine"
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/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
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/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
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|mod_base= OTHER
|not== "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
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mod_base= OTHER
'note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
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                                                                                                   Query Match
1.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                      Oligomer HSV723 for forming triplex with HSV target duplex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag= g
mod_base= OTHER
note= "OTHER= N6 methyl-8-oxo
                                                                                       Sequence 18 BP; 13 A; 0 C; 0 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
treating latent infections e.g. HIV
                Example 4; Page 29; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                             *tag= b
mod_base= OTHER
                                                                                                                                     1590 AAATATAAAAGTAAATAT 1607
                                                                                                                                                     1 AAAAATATATATATAT 18
                                                                                                                                                                                            AAQ30310 standard; DNA; 18
                                                                                                                                                                                                                              (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                              *tag= c
                                                                                                                                                                                                                                                                                                                               *tag= a
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modified_base
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07-DBC-1992
                                                                                                                                                                                                                                                                                               Synthetic
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The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major grove of the duplex. The specific target sequence of this oligomer is a herpes simplex virus I duplex beginning at nuclectide 10996 contg. a purine-rich region concentrated on concentrated on chain of the duplex. The oligomer, and others like it are useful in diagnosis and therapy of diseases characterised by specific DNA duplex targets, e.g. respiratory syncytial virus, HIV, hepatitis, herpes, malignant tumours and inflammation. The triple helices form under mild conditions thus assays may be carried out without subjecting the test specimen to harsh conditions. The oligomer contains an inverted polarity region formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso (mucleotides have the 3 positions of xylose sugars linked via the o-xylene ring). Two contiections are coupled through a xylene residue to form the dimer synthon. This additional modifications may render the oligomer stable to nuclease activity. The oligomer is able to inhibit gene expression, as verified by in vitro systems.

See also AAQ25452-25501 and AAQ30226-448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis, herpes, malignancy and inflammation
                                                                                                                                                                                                                                                                                                                                                                                            /*tag= m
/mcd_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
'note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
                                                                                                                                                                                                                                                                         *tag= 1
|mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
                                                                                                             deoxyadenine
                                                                                                                                                                                                                       deoxyadenine
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                                                                                  /mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "see comments
                                                                                                                                                                  /*tag= k
/mod_base= OTHER
/note= *OTHER= N6
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91US-0643382.
91US-0683420.
91US-0686544.
91US-0686546.
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                                                          /*tag= j
/mod base=
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/label=
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                                   modified base
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18-JAN-1991;
08-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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17-APR-1991;
17-APR-1991;
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OTHER

/mod base=

schultz143-3.rng

Milligan J;

Matteucci MD,

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New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis, herpes, malignancy and inflammation
                                                                                               Claim 12; Page 67; 77pp; English.
27-SEP-1991; 91US-0766733
                                Krawczyk S,
                (GILE-) GILEAD SCI INC.
                                               WPI; 1992-217083/26.
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modified_base
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07-DEC-1992
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                                 Gaps
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'note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
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|mod_base= OTHER
/not== "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
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/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
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/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine'
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/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
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mod_base= OTHER
note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine'
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note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine
                Length 18;
                                                                                                                                                              Oligomer HSV702 for forming triplex with HSV target duplex
                                3; Indels
               Score 13.2; DB 1;
Pred. No. 3.8e+02;
0; Mismatches 3;
Sequence 18 BP; 13 A; 0 C; 0 G; 5 T; 0 other;
                                                                                                                                                                                                                      Location/Qualifiers
                                               1590 AAATATAAAAGTAAATAT 1607
                                                           1 AAAAATAAATAAATAT 18
              ch
l Similarity 83.3%;
15; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-0617907.
91US-0643382.
91US-0683420.
91US-0686544.
91US-0686546.
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                                                                                                       AAQ30302 standard; DNA; 18
                                                                                                                                      25-MAR-2003 (updated)
07-DEC-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      *tag= f
                                                                                                                                                                                                                                                                      *tag= b
                       Local Similarity
                                                                                                                                                                                                                       Key
modified_base
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08-APR-1991;
17-APR-1991;
17-APR-1991;
17-APR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-NOV-1990
                                                                                                                                                                                                      Synthetic
                                                                                                                       AAQ30302;
                Query Match
                               Matches
                                                                                       RESULT 305
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The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major growe of the duplex. The specific target sequence of this oligomer is a herpes simplex virus I target duplex concentrated on one chain of the duplex. The oligomer, and others concentrated on one chain of the duplex. The oligomer, and others like it are useful in diagnosis and therapy of diseases characterised by specific DNA duplex targets, e.g. respiratory syncytial virus, HIV, hepacifits, herpes, malignant tumours and inflammation. The triple helices form under mild conditions thus assays may be carried out without subjecting the test specimen to harsh conditions. The oligomer may contain an inverted polarity region formed from an overload of duper synthom. The linking gp. is o-xyloso (nucleotides have the 3' positions of xylose sugars linked via the o-xylene ring). Two nucleotides are coupled through a xylene residue to form the dimer synthom. This additional modification may render the oligomer stable to muclease activity. The oligomer is able to inhibit gene expression, as verified by in vitro systems. See also AAQX5452-25501 and AAQ30226-448.

(Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human interleukin - 1 beta gene; herpes simplex; AIDS; modified;
HIV; RSV; HPV; malignancy; hepatitis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/mcd_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= b
/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 8 A; 0 C; 0 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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(first entry)
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Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis; precore region; HBSAg region; genotype specific target; mutation detection; ss.

Synthetic. Hepatitis b virus.

WO9740193-A2.

30-0CT-1997

Probe HBPr257 for RT pol region of HBV.

(first entry)

19-MAY-1998

AAV14091;

AAV14091 standard; DNA; 18 BP.

RESULT 307

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The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major grove of the duplex. The specific target sequence of this oligomer is the human interleukin -1 beta gene beginning at nucleotide 6379 contg. a purine rich sequence concd. on one strand of this oligomer, and others like it are useful in diagnosis and therapy of disease characterised by specific DNA diagnosis and therapy of disease characterised by specific DNA duplex targets, e.g. HPV; HER, HIV, hepatitis B, herpes, malignant tumours and inflammation. The triple helices form under mild conditions tumours and inflammation without subjecting the test specimen to harsh conditions. The oligomer contains an inverted polarity region formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso funcleotides have the 3' positions of xylose sugars linked via the co-xylone ring). Two nucleotides are compled through a xylene residue to form the dimer synthon. This additional modifications may render the oligomer stable to nuclease activity. The oligomer is able to inhibit gene expression, as verified by in vitro systems.

See also AAQ25452-25501 and AAQ30226-448.

(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis, herpes, malignancy and inflammation
                                                                                                               /*tag= e
/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
                                                               /mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine'
                                                                                                                                                             13..18
/*teg=
//abds= inverted polarity_region
/note= "see comments"
12..13
/*teg= g
/note= "o-xyloso dimer synthon linkage"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Page 69; 77pp; English
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91US-0643382.
91US-0686342.
91US-0686544.
91US-0686546.
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                                                 /*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GILE-) GILEAD SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-217083/26.
                                 modified base
                                                                                               modified_base
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08-APR-1991,
17-APR-1991,
17-APR-1991,
17-APR-1991,
27-SEP-1991;
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Detection and/or genetic analysis of hepatitis B virus - specifically genotype, preCore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs

Claim 5; Page 32; 80pp; English.

Maertens G, Rossau R, Stuyver L;

WPI; 1997-535867/49.

(INNO-) INNOGENETICS NV

97WO-EP02002.

21-APR-1997;

19-APR-1996;

```
This sequence represents a probe for the RT pol region of hepatitis

b virus (HBV). This sequence can be used in the method of the invention

cor detection and/or genetic analysis of hepatitis B virus (HBV) in a

sample. The method comprises: (a) optionally releasing, isolating or

concentrating polynucleic acids (1) in the sample, and amplifying the

concentrating polynucleic acids (1) in the sample, and amplifying the

concentrating polynucleic acids (1) in the sample, and amplifying the

concentrating polynucleic acids (1) in the sample, and amplifying the

concentrating polynucleic acids (1) with a combination of at least 1

concentrating polynucleic acids (1) with a combination of at least 1

contract and hybridise specifically to mutant carget sequences chosen from

the HBV RT pol gene region, HBV precore region, HBASHG region and/or HBV

concentrations; (a) detecting the hybridis complements or U for T

concentration hybridisation signal(s). The composition can be used to

differential hybridisation signal(s). The composition can be used to

diagnose and/or monitor HBV mutants and/or genotypes in a sample,

concentrations selected by treatment with drugs, e.g. lamivudume and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.1%; Score 13.2; DB 1; Length 18; Best Local Similarity 83.3%; Pred. No. 3.8e+02; Matches 15; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 BP; 7 A; 0 C; 4 G; 7 T; 0 other;
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ID AAV14083 standard; DNA; 18 BP.
XX
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Gaps

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Query Match 1.1%; Score 13.2; DB 1; Length 18; Best Local Similarity 83.3%; Pred. No. 3.8e+02; Matches 15; Conservative 0; Mismatches 3; Indels

1145 TATTITIATTITAGATATT 1162

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Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis; preCore region; HBBAg region; genotype specific target; mutation detection; ss.
                                                                                                                                                                                                         Detection and/or genetic analysis of hepatitis B virus -
specifically genotype, preCore mutations, vaccine escape mutations
and RT gene mutations selected by treatment with drugs
                              Probe HBPr249 for RT pol region of HBV
               19-MAY-1998 (first entry)
                                                                                                                                                             (INNO-) INNOGENETICS NV
                                                                                                                                                                                           WPI; 1997-535867/49.
                                                                          Synthetic.
Hepatitis b virus.
                                                                                                                                              19-APR-1996;
                                                                                                                               21-APR-1997;
                                                                                                 709740193-A2
                                                                                                                 30-0CT-1997
                                                                                                                                                                            Maertens G,
AAV14083
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Stuyver L;

Rossau R,

97WO-BP02002 96EP-0870053

This sequence represents a probe for the RT pol region of hepatitis

b virus (HBW). This sequence can be used in the method of the invention

c for detection and/or genetic analysis of hepatitis B virus (HBW) in a

sample. The method comprises: (a) optionally releasing, isolating or

concentrating polymucleic acids (1) in the sample, and amplifying the

relevant part of a suitable HBW gene in the sample with at least 1

culevant part of a suitable HBW gene in the sample with at least

culevant part of a suitable HBW gene in the sample, and amplifying the

culevant part of a suitable HBW gene in the sample, and amplifying the

culevant part of a suitable HBW gene in the sample with at least

culevant part of a suitable HBW gene in the accentions on a solid

support and hybridis especifically to mutant suggest sequences chosen from

the HBW RT pol gene region, HBW precore region, HBRA region and/or HBW

centype specific target sequences, or their complements or U for T

concloques; (c) detecting the hybrids formed in step (b), and inferring

the HBW genotype and/or mutants present in the sample from the

differential hybridisation signal(s). The composition can be used to

diagnose and/or monitor HBW mutants and/or genotypee in a sample,

specifically genotype, precore mutations and

RT gene mutations selected by treatment with drugs, e.g. lamivudume and Sequence 18 BP; 7 A; 0 C; 4 G; 7 T; 0 other; Claim 5; Page 32; 80pp; English

Gaba ç Query Match 1.1%; Score 13.2; DB 1; Length 18; Best Local Similarity 83.3%; Pred. No. 3.8e+02; Matches 15; Conservative 0; Mismatches 3; Indels

1123 TATAAAGATGTTATAGTA 1140 18 TATATGGATGATATAGTA

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AAV14088 standard; DNA; 18 RESULT 309 AAV14088
ID AAV1
XX
AC AAV1
XX
DT 19-#
XX
XX

AAV14088;

19-MAY-1998 (first entry)

Probe HBPr254 for RT pol region of HBV.

Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis; preCore region; HBsAg region; genotype specific target; mutation detection; ss.

Synthetic. Hepatitis b virus.

409740193-A2

30-0CT-1997.

96EP-0870053 19-APR-1996;

97WO-EP02002.

21-APR-1997;

(INNO-) INNOGENETICS NV

Stuyver L; Maertens G, Rossau R,

4PI; 1997-535867/49

Detection and/or genetic analysis of hepatitis B virus - specifically genotype, preCore mutations, vaccine escape mutations and RT gene mutations selected by treatment with drugs

Claim 5; Page 32; 80pp; English.

This sequence represents a probe for the RT pol region of hepatitis by virus (HBV). This sequence can be used in the method of the invention cor detection and/or genetic analysis of hepatitis B virus (HBV) in a sample. The method comprises: (a) optionally releading, isolating or concentrating polymucleic acids (1) in the sample, and amplifying the cencentrating polymucleic acids (1) in the sample, and amplifying the relevant part of a suitable HBV gene in the sample with at least 1 suitable primer pair; (b) hybridising (1) with a combination of at least 2 nucleotide probes, which are applied to known locations on a solid support and hybridise specifically to mutant target sequences chosen from the HBV RT pol gene region, HBV precore region, HBSA region and/or HBV genotype specific target sequences, or their complements or U for T proposes; (c) detecting the hybrids formed in step (b), and inferring the HBV genotype and/or mutants present in the sample from the differential hybridisation signal (8). The composition can be used to differential hybridisation signal (8). The composition can be used to specifically genotype, precore mutations, vaccine escape mutations and control of the matations selected by treatment with drugs, e.g. lamivudune and Senciclovir.

Sequence 18 BP; 7 A; 1 C; 3 G; 7 T; 0 other;

Gaps ċ Query Match 1.1%; Score 13.2; DB 1; Length 18; Best Local Similarity 83.3%; Pred. No. 3.8e+02; Matches 15; Conservative 0; Mismatches 3; Indels

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RESULT 310

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AAV14089 standard; DNA; 18 BP AAV14089;

19-MAY-1998 (first entry)

Probe HBPr255 for RT pol region of HBV.

Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis; precore region; HBsAg region; genotype specific target; mutation detection; ss.

Synthetic. Hepatitis b virus.

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RESULT 312
AAV36356/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             음
                                                                                                                                                                                                                                                                                             This sequence represents a probe for the RT pol region of hepatitis be virus (HBV). This sequence can be used in the method of the invention for detection and/or genetic analysis of hepatitis B virus (HBV) in a sample, The method comprises: (a) optionally releasing, isolating or concentrating polymucleic acids (I) in the sample, and amplifying the releast part of a suitable HBV gene in the sample with at least 1 suitable primer pair; (b) hybridising (I) with a combination of at least 2 nucleotide probes, which are applied to known locations on a solid 2 nucleotide probes, which are applied to known locations on a solid 2 nucleotide probes, which are applied to known locations on a solid 2 nucleotide probes, which have recore region, HBSA region and/or HBV genotype specific target sequences, or their complements or U for T concloques; (c) detecting the hybrids formed in step (b), and inferring the HBV genotype and/or mutants present in the sample from the differential hybridisation signal(s). The composition can be used to diagnose and/or monitor HBV mutants and/or genotypes in a sample, specifically genotype, precore mutations and or monitor HBV mutants and/or decore mutations and RT gene mutations selected by treatment with drugs, e.g. lamivudune and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                              Detection and/or genetic analysis of hepatitis B virus -
specifically genotype, preCore mutations, vaccine escape mutations
and RT gene mutations selected by treatment with drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5'-flanking region; PCR primer; analysis; enetic screening; endothelial nitrogen monoxide synthase; eNOS; genetic screening; coronary arterial spasm; angina pectoris; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 18
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Pred. No. 3.8e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sense primer 1 for eNOS gene 5'-flanking region (-786)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 BP; 7 A; 0 C; 3 G; 8 T; 0 other;
                                                                                                                                                         Maertens G, Rossau R, Stuyver E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATAAAGATGTTATAGTA 1140
                                                                                                                                                                                                                                                                        Claim 5; Page 32; 80pp; English
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                                                                     97WO-BP02002
                                                                                                  96EP-0870053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.39
Matches 15; Conservative
                                                                                                                              (INNO-) INNOGENETICS NV
                                                                                                                                                                                    WPI; 1997-535867/49.
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                                                                                                 19-APR-1996;
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                                                                       21-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9718327-A1
               WO9740193-A2
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                                          30-OCT-1997
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Gaps
                                                                                                                                                                                                                                                                     The present sequence is a primer for the PCR amplification of the endothelial nitrogen monoxide synthase (eNOS) gene 5'-flanking region (-1468). The amplification product was used in an example of genetic screening method for diseases associated with coronary arterial spasm, which comprises determining if 1 or more specific nucleotides in the eNOS gene have been substituted, specifically G894T, C774T, T(-786)C, A(-922)G and T(-1468)A. Screening for diseases associated with coronary spasm, e.g angina pectoris, cannot be easily carried out by existing methods, this method allows rapid and easy detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense oligonucleotide HAdA3MM1, targeting adenosine A3 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secondary structure; mRWh; phosphorothioate backbone; G-protein; bronchoconstriction; lung inflammation; asthma; pulmonary disease; allergy; emphysema; cystic fibrosis; ss.
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                                                                                                                                                               Genetic screening for diseases associated with coronary arterial spasm - by assessment of the occurrence of specific mutation(s) the endothelial nitrogen monoxide synthase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 13.2; DB 1; Length 18 Pred. No. 3.8e+02; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 1 A; 1 C; 7 G; 9 T; 0 other;
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                                                                                                                                                                                                                                             Example 7; Page 26; 47pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1355 GTGTTGGTAGTGCTGTGT 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGGTTTGTAGTTCTGTGT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV36356 standard; DNA; 18 BP
28-JUN-1996; 96JP-0168761.
13-NOV-1995; 95JP-0319504.
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Best Local Similarity 83.3%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                       SHIO ) SHIONOGI & CO LID
                                                                                           Fasue H, Yoshimura M;
                                                                                                                               WPI; 1997-289303/26
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV36356;
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Disclosure, Page 20; 54pp; English.

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G protein-coupled receptor kinase 4 mutants associated with essential hypertension, useful for identifying anti-hypertensive
                                                                                                                                                                                                                                                                   (GEOU ) UNIV GEORGETOWN MEDICAL CENT. (UYVI-) UNIV VIRGINIA PATENT FOUND.
                                                                                                                                                                                                                                                                                         WPI; 1999-444199/37
                                                                                                                                                                                                                                                                                 Relder R, Jose P;
                                                                                                                                                                                                                                                        28-AUG-1998;
12-JAN-1998;
                                                                                                                                                                                                                                               12-JAN-1999;
                                                                                                                                                                                                                      Homo Bapiens
                                                                                                                                                                                                                              409935279-A1
                                                                                                                                                                                                                                       15-JUL-1999.
                                                                                                                                                                                                                 Synthetic
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The present invention describes an isolated nucleic acid molecule encoding a G protein-coupled receptor kinase (GRK) 4 protein having an R651, A142v A186v A165v, A162v, A165v, A16v, A16v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAY-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX57900
g
                                                                                                                                                                                                                                                                                                                                                      Sequences AAV36356 and AAV36358 are anti-sense oligonucleotides used as mismatched controls to target the human adenosine A3 receptor and thus test the other oligonucleotides, AAV36355 and AAV36357 respectively, the design of which required the secondary structure was both analysed and used to construct antisense oligonucleotides containing a phosphorothioate backbone. Once the antisense molecules are created they can be used to target their predetermined sequence, thus causing the test can be used to decrease. The antisense oligonucleotides were targeted they can be used to decrease. The antisense oligonucleotides were targeted to specific many average their approach to decrease. The antisense oligonucleotides were targeted is a member of the G-protein coupled family of cell surface receptors is a member of the G-protein coupled family of cell surface receptors to treat or prevent conditions associated with bronchoconstriction and/or lung inflammation in humans or other animals e.g. asthma, pulmonary disease, allergy, emphysema and cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                          Treating respiratory disease with antisense sequences directed against adenosine or bradykinin receptors - with localised delivery to the respiratory system, suitable for long term treatment of asthma, adult respiratory distress syndrome etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13.2; DB 1; Length 18;
Pred. No. 3.8e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 18 BP; 3 A; 4 C; 6 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                         Example 1; Page 30; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   869 GCCAGGATCCACAAGTCC 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRK4 allele specific probe #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX90242 standard; DNA; 18 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.1%;
Best Local Similarity 83.3%;
Matches 15; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 GCCATGATCCGCAAGTAC
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                                                                                                                                                                                                                                                                    AcmA repeat; consensus sequence; major peptidoglycan hydrolase; vaccine; cell wall attachment; substance delivery; diagnosis; bioadsorption;
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a PCR primer used in the construction of acm4 derivatives. The invention relates to a proteinaceous substance that comprises at least one stretch of amino acids derived from a first organism, capable of attaching to a cell wall of a second microorganism. The proteinaceous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New proteinaceous substance comprising a sequence consensus to a major peptidoglycan (AcmA), useful for attaching a substance to a cell wall
                             ö
  Length 18;
                            3; Indels
Score 13.2; DB 1;
Pred. No. 3.8e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                         PCR primer for construction of AcmA derivatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Page 18; 98pp; English.
                                                        502
                                                                        1 TGTTGTAGGACTGCCTGA 18
                                                                                                                                                       AAX57900 standard; DNA; 18 BP.
1.1%;
ilarity 83.3%;
Conservative
                                                      484 TGTTGTAGGGTTGCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                            97EP-0203539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYGR-) RIJKSUNIV GRONINGEN
                                                                                                                                                                                                              15-JUL-1999 (first entry)
             Local Similarity
nes 15; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-290024/25.
                                                                                                                                                                                                                                                                                              PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                         13-NOV-1997;
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98US-0098279. 99WO-US00663

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Page 158

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cc substance is useful in a method for attaching a substance to the cell wall of a microorganism, and the substance and either microorganism are useful in pharmaceutical compositions and vaccines, for delivery of a substance to a cell. They are also useful in diagnostic tests, constanted to constant and in foodstuffs. The new method targets bloadscrotton processes and in foodstuffs. The new method targets ambatances to cells of a wide range of microorganisms, unlike prior art and nardeting proteins which are specific and selective for a limited set of microorganisms, which are usually recombinant or consensus, preventing restrictions on applications, and preventing consential problems of colonisation of the mucosal surfaces which can ceause immune tolerance. Public consensus is against use of recombinant or attenuated strains, so the new technique is more likely to be accepted than prior art methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYP3A4 gene polymorphism; polymorphic locus; human; altered metabolism; CYP3A4 substrate; drug-drug interaction identification; toxin exposure; genetic linkage detection; phenotypic variation; promoter; PCR primer;
                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                               1.1%; Score 13.2; DB 1; Length 18; 33.3%; Pred. No. 3.8e+02; ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                    Sequence 18 BP; 7 A; 2 C; 2 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer for Human CYP3A4 gene promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated CYP3A4 polymorphic sequences
                                                                                                                                                                                                                                                                                                                                              1313 AACAATCCTAGTTTGATA 1330
                                                                                                                                                                                                                                                                                                                                                                1 AGCAATACTAGTTTTATA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX28308 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AXYS-) AXYS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guida M, Lichter JB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-215070/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9913106-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX28308;
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 315
AAX28308
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This sequence represents a PCR primer for the human CYP3A4 gene promoter. The invention relates to a CYP3A4 sequence polymorphism, which is part of a non-naturally occurring chromosome. Nucleic acids comprising the CYP3A4 polymorphic sequences can be used to screen partents for altered metabolism for CYP3A4 substrates, potential drug-drug interactions, and adverse/side effects as well as diseases that result from environmental or occupational exposure to toxins. They can also be used to establism animal, call culture and in vitro cell-free models for drug metabolism. Polymorphic CYP3A4 gene sequences can be used for expression studies to determine the effect of promoter and/or intron

Example; Page 18; 40pp; English

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sequence variations on mRNA expression and stability. The polymorphisms are also used as single nuclectide polymorphisms to detect genetic linkage to phenotypic variation in activity and expression of CYP3A4. The nucleic acids can also be used to generate genetically modified non-human animals or site specific gene modifications in cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ7740 represent amplification primers for the biallelia markers. The biallelia markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as weil as other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel biallelic markers used to construct a high density disequilibrium map of the human genome -
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human biallelic marker upstream amplification primer SEQ ID NO:5436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
                                                                                                                                                                                   ö
                                                                                                                                               Ouery Match 1.1%; Score 13.2; DB 1; Length 18; Best Local Similarity 83.3%; Pred. No. 3.8e+02; Matches 15; Conservative 0; Mismatches 3; Indels
                                                                                                            Sequence 18 BP; 10 A; 2 C; 6 G; 0 U; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chumakov
                                                                                                                                                                                                                          414 CAAGAATCAGTGAAGATG 431
                                                                                                                                                                                                                                                    1 CAAGAAACAGAGAAGAGG 18
                                                                                                                                                                                                                                                                                                                                                         AAZ71080 standard; DNA; 18 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI, 2000-013267/01
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23-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                AAZ71080;
                                                                                                                                                                                                                                                                                                                     RESULT 316
AAZ71080/c
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Type III secretion; Yersinia; YopB; YopN; Yop protein; phagocytic; macrophage; antisense; ss.

Yersinia enterocolitica, Synthetic,

KO9960011-A1

25-NOV-1999.

99WO-US11361.

21-MAY-1999; 21-MAY-1998;

980S-0086302.

Schneewind O, Anderson DM;

WPI; 2000-072427/06.

(REGC) UNIV CALIFORNIA.

ersinia YopE spontaneous suppressor mutant fragment.

(first entry)

17-MAR-2000

AAZ40683;

AAZ40683 standard; RNA; 18 BP.

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                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Type III secretion; Yersinia; YopB; YopN; Yop protein; phagocytic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense oligonucleotide inhibition useful for suppression ovirulence and improvement of host defense mechanisms such as
1.1%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 3.8e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
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Pred. No. 3.8e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 28; 50pp; English
                                                                   .,
                                                                                                                                               421 CAGTGAAGATGCCAGTGA 438
                                                                                                                                                                                                               CAGTGAAGGTGTCAGTTA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US11361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yersinia Yopk mRNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0086302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schneewind O, Anderson DM;
                                                                                                                                                                                                                                                                                                                                                                                            AAZ40682 standard; RNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    macrophage; antisense; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAR-2000 (first entry)
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yersinia enterocolitica.
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Best Local Similarity
Matches 15; Conserv
                                     Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phagocytosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ40682;
                                                                                                                                                                                                               18
   Query Match
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XX AAZ4

AAZ4
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Antisense oligomucleotide inhibition useful for suppression of virulence and improvement of host defense mechanisms such as

Disclosure; Page 28; 50pp; English.

phagocytosis -

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method of inhibiting Type III secretion of proteins by Yersinia by contacting the cell with an antisense oligo that binds at least a portion of mRNA encoding the first 15 amino acids of either the wild-type YopB or YopN protein. The methods are useful for inhibiting Type III secretion of proteins by Yersinia (especially Yop proteins which allow Yersinia to evade phagocytic killing by macrophages) and other Gram-negative bacteria, where the antisense oligonucleotide binds a portion of mRNA encoding a secretion signal of a secreted protein of a Gram-negative bacterium. The Gram-negative bacterium that can be targeted include Yersinia spp., Bscherichia coli, Salmonella spp., Shigella spp., Pseudomonas spp. and Xanthomonas spp. Inhibiting Type III secretion of proteins is useful for enhancing a hosts defenses against compounds, which block or inhibit the type III secretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            !ype III secretion; Yersinia; YopE; YopN; Yop protein; phagocytic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.1%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 3.8e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yersinia Yopk spontaneous suppressor mutant fragment.
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Conservative
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AAZ40684 standard; RNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           macrophage; antisense; ss.
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mes 15; Conserv
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RESULT 318 AAZ40683/c

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(REGC ) UNIV CALIFORNIA.
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AAD17638/
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                                                                                                                                                                                                                                      The invention relates to a method of inhibiting Type III secretion of proteins by Yersinia by contacting the cell with an antisense oligo that binds at least a portion of mRNA encoding the first 15 amino acids of either the wild-type Yops or YopN protein. The methods are useful for inhibiting Type III secretion of proteins by Yersinia (especially Yop proteins which allow Yersinia to evade phagocytic killing by macrophages) and other Gram-negative bacteria, where the antisense oligonucleotide binds a portion of mRNA encoding a secretion signal of a secreted protein of a Gram-negative bacterium. The Gram-negative bacterium is a secreted protein targeted include Yersinia spp. Bscherichia coli, Salmonella spp., Scherichia coli, Salmonella spp., secretion of proteins is useful for enhancing a hosts defenses against such bacteria. The methods also provide a means for screening for compounds, which block or inhibit the type III secretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Type III secretion; Yersinia; YopE; YopN; Yop protein; phagocytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                            Antisense oligonucleotide inhibition useful for suppression of virulence and improvement of host defense mechanisms such as
                                                                                                                                                                                                                                                                                                                                                                                                                    ch 1.1%; Score 13.2; DB 1; Length 18; I Similarity 83.3%; Pred. No. 3.8e+02; 15; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yersinia YopE spontaneous suppressor mutant fragment
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 BP; 9 A; 2 C; 1 G; 6 U; 0 other;
                                                                                                                                                                                                                      Disclosure, Page 28; 50pp; English
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                                                                          99WO-US11361
                                                                                              98US-0086302
                                                                                                                                       Schneewind O, Anderson DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ40685 standard; RNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   macrophage; antisense; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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    Yersinia enterocolitica
                                                                                                                 (REGC ) UNIV CALIFORNIA
                                                                                                                                                          WPI; 2000-072427/06
                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 15; Conserv
                                                                          21-MAY-1999;
                                                                                              21-MAY-1998;
                                                                                                                                                                                                    phagocytosis
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                                WO9960011-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAY-1998;
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              Synthetic.
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The invention relates to a method of inhibiting Type III secretion of proteins by Yersinia by contacting the cell with an antisense oligo that binds at least a portion of mRNA encoding the first 15 amino acids of either the wild-type Yopk or YopN protein. The methods are useful for inhibiting Type III secretion of proteins by Yersinia (especially Yop proteins which allow Yersinia, where the antisense oligonucleotide binds a portion of mRNA encoding a secretion signal of a secreted protein of a carm-negative bacterium. The Gram-negative bacterium is secreted protein of a carm-negative bacterium. The Gram-negative bacterium for Shigella spp., Schlerichia coli, Salmonella spp., Shigella spp., Redendomonas spp. and Xanthomonas spp. Inhibiting Type III secretion of proteins is useful for enhancing a hosts defenses against compounds, which block or inhibit the type III secretion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                             Antisense oligonucleotide inhibition useful for suppression of virulence and improvement of host defense mechanisms such as phagocytosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 1.1%; Score 13.2; DB 1; Length 18; Local Similarity 83.3%; Pred. No. 3.8e+02; les 15; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human GCPII gene exon-4 amplifying PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 18 BP; 9 A; 2 C; 0 G; 7 U; 0 other;
                                                                                                                                                                                                                                                                                         Disclosure; Page 28; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1160 ATTAAATGATGTTTTATT 1177
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AAD17638 standard, DNA; 18 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-2001; 2001WO-US07880.
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Schneewind O, Anderson DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                          WPI; 2000-072427/06.
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The patent discloses methods for screening an individual for increased risk of low folate status. The method involves detecting a mutation in the human glutamate carboxypeptidase (GCP) I gene in a biological sample from said individual, wherein detection of the mutation is indicative of decreased ability of an individual to hydrolyse terminal glutamate residues from dietary folates by folypoly-gamma-djutamate carboxypeptidase (FGCP), a product of GCPII gene. The decreased ability is associated with low folate status. The method is useful for screening an individual for increased risk of low folate status and conditions an individual for increased risk of low folate status and conditions cancer and altered cognition in the elderly including Alzheimer's disease. Pregnant women with low folate status are at increased risk of bearing children with neural tube defects and congenital heart defects. The present DNA sequence is a PCR primer which is used for amplifying exon-4 of GCPII gene. This primer is designed from PSNA genomic sequence and is used for detecting a mutation in GCPII gene.
                                   Example 5, Page 26, 38pp; English.
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Seguence 18 BP; 7 A; 3 C; 2 G; 6 T; 0 other;

1.1%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 3.88+02; tive 0; Mismatches 3; Indels 1230 CAGTTAAATTTTCATTTC 1247 18 CAGTTAAAGTTTGATTAC Query Match Best Local Similarity 83.3 Matches 15; Conservative ð 윤

RESULT 322

AAH26220 standard, DNA; 18

AAH26220;

(first entry) 17-SEP-2001 Parathyroid hormone cDNA 3' PCR primer.

Parathyroid hormone; parathormone; PTH; kidney failure; rat; osteoporosis; gene therapy; ss.

Rattus sp.

WO200149838-A2.

12-JUL-2001

02-JAN-2001; 2001WO-IL00006

03-JAN-2000; 2000IL-0133875

(HADA-) HADASIT MEDICAL RES SERVICES & DEV.

Silver J, Naveh T;

WPI; 2001-432876/46.

Novel isolated cis-acting regulatory nucleic acid sequence comprising 3'-untranslated region of parathyroid hormone gene useful in gene therapy for treating pathological condition such as chronic renal therapy

Example 1; Page 39; 83pp; English.

The present sequence is that of a 3' PCR primer used in the amplification of a 40 nucleotide transcript, which was used in the construction of a plasmid containing rat parathyroid hormone (PTH) cDNA. Cis-acting sequences (see AAH26198-211) comprising fragments of the 3' untranslated region of mammalian PTH genes, or allelic variants, mutants or functionally equivalent

fragments, can be linked to a heterologous or homologous coding sequence of interest, and direct specific regulation of stability of the mRNA encoded by the linked coding sequence. The regulation of the stability of the mRNA is responsive to changes in serum levels of any one of calcium and phosphate and is further mediated by the binding of at least one parathyroid protein or its derivatives to the cis-acting sequence. A pharmaceutical composition for the cis-acting sequence. A pharmaceutical composition for the cis-acting sequence. A pharmaceutical composition for function of the parathyroid gland or abnormal metabolism of calcium and/or phosphate comprises parathyroid protein or an agent that binds to the cis-acting element. It is useful for preventing and/or treating over- or underproduction of PTH, bone diseases, contracting over- or underproduction of PTH, bone diseases, and for treating sequence with a coding sequence is useful in gene therapy. 88888888888888888888

Sequence 18 BP; 10 A; 1 C; 2 G; 5 T; 0 other;

Gaps ö Length 18; 3; Indele Score 13.2; DB 1; Pred. No. 3.8e+02; 0; Mismatches ch 1.1%; il Similarity 83.3%; 15; Conservative Query Match Best Local Similarity Matches 15; Conserv

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Gaps

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RESULT 32: AAH63112/

AAH63112 standard; DNA; 18 BP

AAH63112;

(first entry) 11-SEP-2001

Shrimp white spot Bacilliform virus (WSBV) oligonucleotide 273.

Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection; antiviral agent; gene expression; antisense construct; probe; primer; transgenic viral resistant shrimp; ss.

White spot syndrome virus.

40200138351-A2

31-MAY-2001.

08-NOV-2000; 2000WO-US28888

99CN-0124717 24-NOV-1999;

THIRD INST OCEANOGRAPHY STATE OCEANI C A. (SINO-) SINOGENOMAX CO (PENY-) PE CORP NY.

Kodira Shen Y, Ye Y, He M, Yang F, He J, Pham L, Κu Χ,

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WPI; 2001-355877/37.

8 Primary nucleotide sequence of the shrimp white spot Bacilliform (WSBV), useful for producing viral polypeptides that can be used screen for agents that are useful for treating WSBV infection -

Disclosure, Figure 3; 626pp, English.

genome The invention provides the primary nucleotide sequence of the WSBV genome (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and encoded proteins (AAG84010-AAG85051) and oligonucleotide sequences (AAH62840-63160) suitable for use as primers or probes. The nucleic acid molecules and proteins of the invention are useful for diagnosis and monitoring viral infection, in screens for antiviral agents and for monitoring viral gene expression or activity during a treatment regimen. The nucleic acid molecules are also useful as antisense constructs to

BP.

(first entry)

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The present invention describes a method of producing binary sequence tags from nucleic acid fragments in a sample, involving incubating the sample with cleaving reagents, mixing offset adaptors with the sample, incubating with more cleaving reagents and mixing the sample with adaptor-indexers where the adaptors are coupled to binary sequence tags. The method is useful in sequence analysis, including analysis and comparison of gene expression, nucleic acid samples and genomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing binary sequence tags, useful for analyzing nucleic acid sequence tags, gene expression or gene-expression patterns, involves generating nucleic acid fragments, which are mixed with offset adaptors and adaptor-indexers
                                                                                                                                                                                                                                                   Binary encoded sequence tag; BEST; nucleic acid analygis; gene expression; adaptor; PCR primer; ss.
                                                                                                                                                                                                   Binary encoded sequence tag method anchored primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 100; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-AUG-2000; 2000WO-US22164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1999; 99US-0148870.
06-APR-2000; 2000US-0544713.
                                          AAF75597 standard; DNA; 18
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                                                                                                                                                   10-MAY-2001
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                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                   AAF75597;
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RESULT 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is one of a number of antisense compounds of up to 30 rucleobases in length targeted to a nucleic acid encoding human Akt-3. The antisense compounds are useful for inhibiting the expression of human Akt-3 in human cells or tissues. They are also useful for modulating the expression of Akt-3, and for treating a human or an animal suspected of having, or being prone to, a disease or condition associated with Akt-3 expression. The antisense compounds may also be used as research reagents, in kits and in diagnostics, e.g. to elucidate the function of a particular gene or to distinguish between functions of various members of a biological pathway; and as a prophylactic, e.g. to prevent or delay infection, inflammation or tumour formation.
                                                                                                                                                                                  ö
gene expression in infected cells and tissues and to create
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, Akt-3; protein kinase; cytostatic, antiinflammatory; infection; antisense therapy; inflammation; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense compounds targeting nucleic acids encoding human Akt-3 useful for treating a disease or condition associated with Akt-3 expression, or in preventing or delaying inflammation or tumor
                                                                                                                                                                                     Gaps
                                                                                                                                                                                     ö
                                                                                                                                  Length 18;
                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Akt-3 antisense oligonucleotide, SEQ ID NO: 81.
                                                                                                                         1.1%; Score 13.2; DB 1; ilarity 83.3%; Pred. No. 3.8e+02; Conservative 0; Mismatches 3;
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                                                                            Sequence 18 BP; 6 A; 5 C; 2 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Column 40; 37pp; English.
                               transgenic viral resistant shrimp
                                                                                                                                                                                                                                                                                                                                                                     RESULT 324
AAF79673/C
ID AAF79673;
XX
AC AAF79673;
XX
C 29-MAY-2001 (first entry)
XX
Human Akt-3 antisense oligonuclec
XX
Human Akt-3; protein kinase; cyl
XM
Antisense therapy; inflammation;
XX
Homo sapiens.
XX
Homo sapiens.
XX
Homo sapiens.
XX
C 29-DEC-1999; 99US-0474922.
XX
XX
C 29-DEC-1999; 99US-0474922.
XX
XX
MP1; 2001-264979/27.
XX
MP1; 2001-264979/27.
XX
MP1; 2001-264979/27.
XX
XX
MP1; 2001-264979/27.
XX
XX
New antisense compounds targeting pr
T useful for treating a disease or expression, or in preventing or of a compound of a compound
                                                                                                                                                                                                                                           1073 ALTIGIGCAAGAATTIGG 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roth RA;
                                                                                                                                                                                                                                                                                           18 Arcrerecadeararred 1
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Best Local Similarity 85...
Best Local Similarity 85...
                                                                                                                                                Local Similarity
es 15; Conserv
control viral
                                                                                                                                     Query Match
                                                                                                                                                                                     Matches
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Latimer DR

Feng L,

Lizardi PW,

Roth ME,

99US-0148870.

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ö
                                                                                                                                                                                                                                                   Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme; detection; mutation; anti-HIV drug resistance; polymorphism; resistance;
                                              Gaps
                                                                                                                                                                                                                           HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:9.
                                              ö
                     Score 13.2; DB 1; Length 18; Pred. No. 3.8e+02;
                                              3; Indels
Seguence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 other;
                                               0; Mismatches
                                                                                                                                                                                                                                                                                                     Ruman immunodeficiency virus type 1.
                                                                      616 ACAAAAAACAACAAATAA 633
                                                                                             Н
                                                                                                                                                          ם
                         1.18;
83.38;
                                                                                                18 ACAAAAAAAAAAAAAA
                                                                                                                                                 767/c
ABZ33767 standard; DNA; 18
                                                                                                                                                                                                        (first entry)
                                    1 Similarity 83.3
                                                                                                                                                                                                         31-JAN-2003
                                                                                                                                                                                                                                                                                ргоре; вв.
                                                                                                                                                                                                                                                                                                                   Synthetic
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Gaps

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Length 18;

Score 13.2; DB 1; Length 1 Pred. No. 3.8e+02; 0; Mismatches 3; Indels

1.1%;

1596 AAAAGTAAATATGAAACA 1613

ઠે 셤

18 AAAAGAAATTATGAGACA

WO200255741-A2

schultz143-3.rng

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The present invention describes a method for detecting mutations associated with anti-HIV drug resistance in a patient by detecting at least one of the mutations K103N/R, V106A/I/L, V18ICI, MISBUYI, Y18BL, G190A/S/R, T215Y/F/D/S/A and/or O151M/L in the reverse transcriptase (RT) of HIV strains in a biological sample using a specific set of probes of the function together in a reverse-hybridiastion assay. The method and the nucleic acid sequences used in the method are useful for determining viral mutations and/or polymorphisms in the HIV RT gene associated with resistance. The probes are useful for the genetic detection, preferably in vitro detection of the mutations K103N/R, V106A/I/L, Y18IC/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or the mutation is associated with anti-HIV drug resistance. The method provides a rapid, reliable and precise assay or determination and monitoring of antiviral drug resistance or mutations associated with crepresent HIV RT sequences and probes which are used in the expression of the present invention.
                                                                                                                                                                                                                                                                                                         Detecting mutations associated with anti-HIV drug resistance comprises detecting at least one of the mutations in the HIV reverse transcriptase gene by using probes optimized to function together in a reverse-hybridization assay —
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 BP; 11 A; 2 C; 2 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 9; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 TACTGTTACTGATTTTT 1
                                                                                                          11-JAN-2001; 2001EP-0870005.
20-APR-2001; 2001EP-0870085.
24-APR-2001; 2001US-286102P.
                                                                         09-JAN-2002; 2002WO-EP00153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 83.3.
There 15; Conservative
                                                                                                                                                                                          (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                                                 Stuyver L;
                                                                                                                                                                                                                                                                    WPI; 2002-590680/63.
                                    18-JUL-2002
                                                                                                                                                                                                                               De Smet K,
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Gape
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1.1%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 3.8e+02; ative 0; Mismatches 3; Indels
                                                                                   1570 TACEGETECEGALTICEAT 1587
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ABL30677 standard; DNA; 18 BP. ABL30677; Human;

21-MAR-2002 (first entry)

Human HLA genotyping oligonucleotide SEQ ID NO 166.

Human; human leukocyte antigen; HLA; genotype; polymorphism; immunogenetic; transplantation; genetic disease; ss.

Homo sapiens.

WO200192572-AL.

06-DEC-2001

01-JUN-2001; 2001WO-JP04662.

01-JUN-2000; 2000JP-0164798

(NISM) NISSHINBO IND INC. (SYST-) SYSTEM RES INC.

Nishida M. Ichihara T, Matsumura Y, Moriya S, Inoko H, Kagiya T,

WPI; 2002-122074/16

Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of individuals e.g. by determining immunogenetic differences when transplanting between them -

Claim 10; Page 124; 345pp; Japanese.

The invention relates to a typing kit for judging human leukocyte antigen (HLA) genotype of a sample by hybridising a substrate on which 10-24 base oligonucletides (AR150512-AR151809) originating in the sequences of genes e.g. belonging to HLA class I antigens on human genome and containing gene polymorphisms as alloantigens have been immobilised as primers for amplification of cleaved mucleic acids relating to gene polymorphisms. The method is useful for judging HLA genotypes of individuals by determining immunogenetic differences before transplanting between them, providing genetic information to decide compatibility of pancraes, tansplantation e.g. of bone marrow, kidney, liver, pancraes, Langerhans islet in pancrees and cornea, susceptibility diagnosis of genetic diseases and identifying individuals.

Sequence 18 BP; 5 A; 2 C; 4 G; 7 T; 0 other;

Gaps ö 1.1%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 3.8e+02; tive 0; Mismatches 3; Indels Local Similarity 83.3 Query Match Best Loc Matches

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Š 셤 ABX79935 standard; cDNA; 18 ABX79935;

RESULT 328

8

EST polymorphic DNA repeat polynucleotide #260. 17-APR-2003 (first entry)

ö

BST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POMPOI Rep-X; human; genetic disease, drug-treatment; Machado-Joseph; Haw River syndrome; Huntingfon's disease; fragile-X syndrome; Predreich's ataxis; myctonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

Homo sapiens

US6472154-B1

99US-0475947. 31-DEC-1999;

29-OCT-2002.

99US-0475947 31-DEC-1999; (TEXA) UNIV TEXAS SYSTEM.

Wren JD, Minna JD, Fondon JW; Garner HR.

4PI; 2003-208818/20

Identifying a candidate polymorphic repeat within a coding sequence, for understanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for polymorphic probability -

Examples; Column 1093; 588pp; English

The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, BST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat in the computational methods (polymorphic cuseful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to understand, treat or eliminate genetic diseases, predispositions or adverse drug-treatment reactions. Examples of diseases, linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Fredrach's ataxis, myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and spinocerebellar ataxia. The sequences presented in human ESTS.

Sequence 18 BP; 5 A; 2 C; 5 G; 6 T; 0 other;

Ouery Match 1.1%; Score 13.2; DB 1; Length 18; Best Local Similarity 83.3%; Pred. No. 3.8e+02; Matches 15; Conservative 0; Mismatches 3; Indels 836 819 CTGGAAATCCTGGATTTT ð

crecaagacaregarrr 18 9

RESULT 329

ABZ10470 standard; DNA; 18 BP ABZ10470;

16-JAN-2003 (first entry)

Haematopoietic cell proliferation disorder related oligonucleotide #610.

Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; probe; primer; 88.

sapiens Homo

Synthetic.

03-OCT-2002.

WO200277272-A2

26-MAR-2002; 2002WO-EP03401.

26-MAR-2001; 2001US-278333P.

(EPIG-) EPIGENOMICS AG.

Howe A, Mueller J; G, Lesche R, Leu E; Mueller V, Otto T; Berlin K, Braun A, Distler J, Guetig D, Olek A, Piepenbrock C, Adorjan P, Grabs (Lewin A, Lipscher B, Maier S, Model F, I Pelet C, Schwope I, Ziebarth H;

WPE; 2003-018942/01.

Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides -

The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a bological sample obtained from the subject with at least 1 reagent, which distinuishes between methylated and non-methylated CpG dimucleotides within the target nucleic acid. ABZ09861 to ABZ01818 represent specifically claimed nucleotide sequences from the present invention can be used: for invention. Oligomicleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia, as probes for determining the cyrosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder complements; and as primers for the ampliteration of haematopoietic cell proliferation disorder related manipulation of haematopoietic cell proliferation disorder related on the seading a predisposition to, differentiation between the subjectic cell proliferation disorder related consultations; processed from the present invention can also be used for detecting a predisposition to, differentiation between the haematopoietic cell proliferative disorders. The present method enables hamply specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables and disorders allowing for improved and informed treatment of patients.

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Page 45; 117pp; English.

Claim 15;

Sequence 18 BP; 7 A; 0 C; 4 G; 7 T; 0 other;

Gaps ; 0 1.1%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 3.8e+02; ative 0; Mismatches 3; Indels Local Similarity 83.3 ses 15, Conservative Query Match Matches

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1457 GTTTATTATGTACAATA 1474

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Gaps

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ABC00856 standard; DNA; 13 BP.

ABC00856;

(first entry) 20-PBB-2002 Oligonuclectide SEQ ID NO 847 for detecting SNP ISC0000279.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DE-1019173

(BPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C,

Berlin K;

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 847; 29pp + Sequence Listing; German.

This invention describes novel oligonuclectide primers or peptide nucleic

acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABCO0010-ABG29303, ABF00010-ABF99989, ABMO010-ABF99989 and ABCO0010-ABG29989 and ABCO0010-ABG29989 and become the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed especification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences. 88888888888888

Sequence 13 BP; 2 A; 0 C; 2 G; 9 T; 0 other;

Gaps ö Length 13; O; Indels 1.0%; Score 13; DB 1; Le 100.0%; Pred. No. 3.1e+02; tive 0; Mismatches 0; Query Match Best Local Similarity 100.0° Matches 13; Conservative

₹ 셤 RESULT 331

ABC00857 standard; DNA; 13 BP. ABC00857;

(first entry) 20-FEB-2002 Oligonucleotide SEQ ID NO 848 for detecting SNP TSC0000279.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-0CT-2001

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DB-1019173.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C,

Berlin K;

WPI; 2001-657177/75.

set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single nuclectide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 848; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, azdiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation.

ABC00010-ABC99999, ABP00010-ABP99999, ABH00010-ABH999999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences. ABCOOBS 7

ABCOOC ABCOCC ABCO

Sequence 13 BP; 9 A; 2 C; 0 G; 2 T; 0 other;

Gaps ö Length 13; 1.0%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 3.1e+02; iive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.0 Matches 13; Conservative

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RESULT 332

ABC02380 ID ABC0

뗪 ABC02380 standard; DNA; 13

ABC02380;

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(first entry) 20-FEB-2002 Oligonucleotide SEQ ID NO 2371 for detecting SNP TSC000941.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DE-1019173.

(RPIG-) RPIGENOMICS AG

Piepenbrock C, olek A,

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status Berlin K; WPI; 2001-657177/75

Claim 1; SRQ ID 2371; 29pp + Sequence Listing; German.

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation statum in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010-ABC9989, ABF00010-ABP9989, ABH00010-ABH99989 and ABI00010-ABHS2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 other;

Gaps ö Length 13; 0; Indels 1.0%; Score 13; DB 1; Le Local Similarity 100.0%; Pred. No. 3.1e+02; Les 13; Conservative 0; Mismatches 0; Query Match Matches

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1133 TTATAGTAAATTT 1145

1 TTATAGTAATTT 13

8

RESULT 333

ABC02381/c ID ABC02381 standard; DNA; 13 BP.

schultz143-3.rng

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Page 166
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0.6-APR-2001; 2001WO-IB00713

WO200177384-A2

18-OCT-2001.

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20-FEB-2002 (first entry)
ABC02381
        OHOR
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37-APR-2000; 2000DE-1019173 (EPIG-) EPIGENOMICS ઠે g ö This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABE9989, about the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in alectronic format from WIPO at fig.wipo.int/pub/published_pct_sequences. SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status .. Oligonucleotide SEQ ID NO 2372 for detecting SNP TSC000941. Match 1.0%; Score 13; DB 1; Length 13; Local Similarity 100.0%; Pred. No. 3.1e+02; es 13; Conservative 0; Mismatches 0; Indels Claim 1; SEQ ID 2372; 29pp + Sequence Listing; German. Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 other; Berlin K; 06-APR-2001; 2001WO-IB00713. 07-APR-2000; 2000DE-1019173. Piepenbrock C, (EPIG-) EPICENOMICS AG WPI; 2001-657177/75. WO200177384-A2 sapiens 18-OCT-2001 olek A,

Query Match

ABC08774;

Oligonucleotide SEQ ID NO 8765 for detecting SNP TSC0002388. 20-FEB-2002 (first entry)

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75

(EPIG-) EPIGENOMICS AG.

ABC08774 standard; DNA; 13 BP. g

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and extosin methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, candiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABF99899, ABF00010-ABF99899 and ABI00010-ABC9989, and ABI0010-ABC9989 and Specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences. SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps 13 Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single nucleotide polymorphisms and cytosine methylation status ö Oligonucleotide SEQ ID NO 8766 for detecting SNP TSC000238B. Watch 1.0%; Score 13; DB 1; bength 13; Local Similarity 100.0%; Pred. No. 3.1e+02; hes 13; Conservative 0; Mismatches 0; Indels claim 1; SEQ ID 8765; 29pp + Sequence Listing; German. Sequence 13 BP; 0 A; 0 C; 2 G; 11 T; 0 other; × Berlin ВÞ 07-APR-2000; 2000DB-1019173. 06-APR-2001; 2001WO-IB00713 ABC08775 standard; DNA; 13 618 AAAAACAACAAA 630 30-FEB-2002 (first entry) 13 AAAAAACAACAAA 1 Piepenbrock C, WPI; 2001-657177/75 WO200177384-A2. Homo sapiens .B-OCT-2001. ABC08775; Query Match olek A, RESULT 335 Matches ABC089775

IID ABC0

XX ABC0

YX ABC0

YX XX ABC0

YX XX SNP;

XX SNP;

XX SNP;

XX HOMO

XX

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acid (PNA) oligomers for detecting single muclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastroincestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABC99999 and the sequence datas for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                  This invention describes novel oligonuclectide primers or peptide nucleic
               Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single nucleotide polymorphisms and cytosine methylation status
                                                                                                                   Claim 1; SBQ ID 8766; 29pp + Sequence Listing, German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13 BP; 11 A; 2 C; 0 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     618 AAAAAACAACAAA 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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1.0%; Score 13; DB 1; Le 100.0%; Pred. No. 3.1e+02; Mismatches 100.08; Pres 0; W 1 AAAAACAACAAA 13 日

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Gaps

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Length 13; 0; Indels

> ABC18132 standard; DNA; 13 BP ABC18132; RESULT 336

Oligonuclectide SEQ ID NO 18139 for detecting SKP TSC0003861. 20-FBB-2002 (first entry)

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB00713

07-APR-2000; 2000DE-1019173

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single nucleotide polymorphisms and cytosine designed to detect methylation status

Claim 1; SEQ ID 18139; 29pp + Sequence Listing; German

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The

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Gaps

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Length 13;

1.0%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 3.1e+02; tive 0; Mismatches 0; Indels

Best Local Similarity 100. Matches 13; Conservative

Query Match

Sequence 13 BP; 6 A; 2 C; 0 G; 5 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
oligomers are also used for detecting cell type differentiation.
ABC0010-ABC99989, ABF0010-ABF99989, ABR00010-ABH99989 and
ABC0010-ABH180773 represent the oligomers described in the invention.
NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABIGORIO-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide SEQ ID NO 18140 for detecting SNP TSC0003861.
                                                                                                                                                                        1.0%; Score 13; DB 1; Length 13;
100.0%; Pred. No. 3.10+02;
tive 0; Mismatches 0; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE39399, ABF00010-ABE93999, ABF00010-ABE99999 and and SABIG0010-ABE182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed appecification, but was obtained in electronic format from WIPO at
                                                       SNP, single nucleotide polymorphism, human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide SEQ ID NO 19126 for detecting SNP TSC0004001.
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABH99989 and ABI00010-ABH99973 represent the oligomers described in the invention. ANOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in alectronic format from WIPO at fip.wipo.int/pub/published_pct_sequences.
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100.0%; Pred. No. 3.1e+02;
trive 0; Mismatches 0;
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XX C 20-FEB-2002 (first entry)

XX C 10-FEB-2002 (first entry)

XX SNP; single nuclectide polymo peptide nucleic acid; cytosin KW C Entral nervous system; gastr XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX PN W0200177384-A2.

XX PN W020177384-A2.

XX PN W020177384-A2.

XX PN W020177384-A2.

XX GFPR-2001; 2001W0-1B00713.

XX GFPR-2001; 2001W0-1B00713.

XX GRIG-) EPIGENOMICS AG.

XX SPR Of-AFR-2000; 2000DB-1019173.

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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                  Piepenbrock C,
                                                                    (EPIG-) EPIGENOMICS AG.
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Berlin K;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (FWA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DWA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABH00010-ABH99999 and ABC0010-ABE99989, ABH00010-ABH99999 and NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SMP) and cytosine methylation status in chemically pretreated genomic DMA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The accounted nervous system, cardiovascular and metabolic disorders. The ABC00010-ABE099999, ABP00010-ABH999999 and ABI00010-ABE099999, ABP0010-ABH999999 and ABI00010-ABE099999, about of the printed specification, but was obtained in electronic format from WIPO at fip.wipo.int/pub/published_pct_sequences.
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Claim 1; SBQ ID 19458; 29pp + Sequence Listing; German.
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1.0%; Score 13; DB 1; La
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0;
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 89; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 27513 for detecting SNP TSC0007650.

(first entry)

20-FEB-2002

ABC27496 standard; DNA; 13 BP.

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RESULT 34
ABC27496/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, carditoraccular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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1.0%; Score 13; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0;
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                          Sequence 13 BP; 3 A; 0 C; 0 G; 10 T; 0 other;
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                                                                                                  1142 ATTITITITIT 1154
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                                                                                                                  Olek A, Piepenbrock C,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytoshism methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

typing, i

Set of oligonucleotides, useful for diagnosis and cell designed to detect single nucleotide polymorphisms and methylation status

Berlin K;

Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG

WPI; 2001-657177/75.

07-APR-2000; 2000DE-1019173. 06-APR-2001; 2001WO-IB00713.

WO200177384-A2. Homo sapiens.

18-OCT-2001.

Claim 1; SEQ ID 27513; 29pp + Sequence Listing; German.

ABIO0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

tp.wipo.int/pub/published_pct_sequences.

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Sequence 13 BP; 3 A; 0 C; 2 G; 8 T; 0 other;
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytoshie methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABL00010-ABH99989 and ShIGOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                     Claim 1; SEQ ID 27767; 29pp + Sequence Listing; German
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Berlin K;
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Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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100.0%; Pred. No. 3.1e+02;
7ative 0; Mismatches 0; Indels
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Matches 13; Conservative
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ABC00010-ABC9989, ABR0010-ABF9989, ABR001010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the wipo.int/pub/published_pct_sequences.
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oligonucleotides are used for diagnosis and/or prognosis of cancer and a
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EXX AAC ABC2

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Length 13;

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Pred. No. 3.1e+02;
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              Pred. No. 3.1e+02;
Mismatches 0;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABE09995, ABF00010-ABE9989, ABH00010-ABH99999 and ABI00010-ABE99995, The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single nucleotide polymorphisms and cytosine methylation status
                                                   Oligonucleotide SEQ ID NO 29525 for detecting SNP TSC0008747.
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                 20-FEB-2002 (first entry)
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les 13; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABE9989, ABF00010-ABE9989, ABF00010-ABE9989, and ABC0010-ABE9989, and the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status

Berlin

Olek A, Piepenbrock C,

WPI; 2001-657177/75

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB00713 07-APR-2000; 2000DE-1019173

18-0CT-2001.

Claim 1; SEQ ID 29526; 29pp + Sequence Listing; German

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Length 13; 0; Indels

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Best Local Similarity

Matches

Query Match

Sequence 13 BP; 9 A; 0 C; 0 G; 4 T; 0 other; ftp.wipo.int/pub/published_pct_sequences.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                  Oligonucleotide SEQ ID NO 30127 for detecting SNP TSC0009112.
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                                                             ABC30110 standard; DNA; 13 BP.
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                                                                                     ABC30110;
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                                                ABC30110
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

#0200177384-A2

Homo sapiens

Oligonucleotide SEQ ID NO 29526 for detecting SNP TSC0008747.

20-FBB-2002 (first entry)

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ABC29509;

ABC29509 standard; DNA; 13 BP

RESULT 351

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligozers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABE99989, ABH00010-ABH99989 and shift of the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fip.wipo.int/pub/published_pct_sequences. designed to detect single nucleotide polymorphisms and cytosine methylation status -Claim 1; SEQ ID 30127; 29pp + Sequence Listing; German. Seguence 13 BP; 9 A; 0 C; 1 G; 3 T; 0 other; 1594 ATAAAGTAAATA 1606 Query Match Best Local Similarity Best Loca Matches ò g

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide SEQ ID NO 30128 for detecting SNP TSC0009112. 1 ATAAAGTAATA 13

Berlin

Set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 30128; 29pp + Sequence Listing; German.

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, entral nervous system, artiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

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ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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tive 0; Mismatches 0;
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ABC37546 standard; DNA; 13 BP

(first entry)

20-FEB-2002

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ABC37546;

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Set of oligonuclectides, useful for diagnosis and cell typing, idesigned to detect single nuclectide polymorphisms and cytosine Oligonuclectide SEQ ID NO 37563 for detecting SNP TSC0011693 Claim 1; SEQ ID 37563; 29pp + Sequence Listing; German Berlin K; 06-APR-2001; 2001WO-IB00713. 07-APR-2000; 2000DE-1019173. Olek A, Piepenbrock C, (BPIG-) EPIGENOMICS AG WPI; 2001-657177/75. designed to detect methylation status WO200177384-A2. Homo sapiens 18-0CT-2001.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABR00010-ABC99899, ABR00010-ABC99899 and ABL00010-ABC99899 and ABC00010-ABC99899, and cell type differentiation. WOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the wipo.int/pub/published_pct_sequences. Seguence 13 BP; 6 A; 0 C; 2 G; 5 T; 0 other;

Gaps ; 0 Query Match
1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels

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                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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rative 0; Mismatches 0; Indels
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  TATAAAGATGTTA
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABR29989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABR29989, ABF00010-ABF99989, ABH00010-ABH99989 and specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic format from WIPO at the vipo.int/pub/published_pct_sequences.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE09999, ABF00010-ABE9999 and ABE000010-ABE09073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                             Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single nucleotide polymorphisms and cytosine methylation status
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                                                                                    Piepenbrock C,
(EPIG-) EPIGENOMICS AG
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                                                                                         olek A,
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Query Match
1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 752 AATGIGATATITG 764 13 AATGTGATATTTG 1 셤

ABC40556 standard; DNA; 13 BP

(first entry) 21-FBB-2002

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 40573 for detecting SNP TSC0012288.

Homo sapiens

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DE-1019173

(EPIG-) BPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, idealgned to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 40573; 29pp + Sequence Listing; German

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABP9989, ABH00010-ABH9989 and ABI0010-ABH9989, ABF00010-ABH9989 and MOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fitp.wipo.int/pub/published_pot_sequences.
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hes 13; Conservative 0; Mismatches 0;
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide SEQ ID NO 40574 for detecting SNP TSC0012288. 21-FEB-2002 (first entry)

ABC40557 standard; DNA; 13 BP.

ABC40557;

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Homo sapiens.

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DE-1019173.

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 40574; 29pp + Sequence Listing; German.

This invention describes novel oligomucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardicvoscullar and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC39989, ABC0010-ABC9989, ABH00010-ABC99989, ABH00010-ABC99989, ABH00010-ABC9989, ABH00010-ABC9989, ABH00010-ABC90030 and NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pot_sequences. schultz143-3.rng

ABC55323 standard; DNA; 13 BP

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                              Length 13;
                                                                      Query Match 1.0%; Score 13; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 3.1e+02; Matches 0; Mismatches 0; Indels
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Sequence 13 BP; 8 A; 0 C; 0 G; 5 T; 0 other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted gencalic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.
ABC00010-ABC99989, ABR00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABG9989, represent the oligomers described in the invention.
NOTE: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Gapa .. Ģ 1.0%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 3.1e+02; strive 0; Mismatches 0; Indels Length 13; 600 TTATTTATTGAA 612 Query Match Best Local Similarity 100. Matches 13; Conservative

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RESULT 361 ABC55323/c

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cartain nervous system, ardiovascribar and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ARC0010-ABR99989, ABR0010-ABR99899, ABR0010-ABR99899 and ABR0010-ABR99899, ABR0010-ABR99989 and halloudle-ABR99989. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, azdiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABH00010-ABH99989 and ABE00010-ABE99989, ABH00010-ABH99989 and SBI00010-ABE99989, ABH00010-ABH99989 and SBI00010-ABH99989 and SBI00010-ABH99989 and ABE00010-ABH99989 and ABE00010-ABH99989 and SBI00010-ABH99989 and ABE00010-ABH99989 and ABE00010-ABH999 Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status Claim 1; SEQ ID 61535; 29pp + Sequence Listing; German. Berlin K; 06-APR-2001; 2001WO-IB00713. 07-APR-2000; 2000DE-1019173 Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG. WPI; 2001-657177/75. WO200177384-A2 18-OCT-2001

/ Match 1.0%; Score 13; DB 1; Length 13; Local Similarity 100.0%; Pred. No. 3.1e+02; les 13; Conservative 0; Mismatches 0; Indels 1144 TIATTITATITA 1156 Query Match Matches

Sequence 13 BP; 3 A; 0 C; 0 G; 10 T; 0 other;

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ABC61519 standard; DNA; 13 BP. RESULT 363

21-PEB-2002 (first entry)

SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide SEQ ID NO 61536 for detecting SNP TSC0016371.

Homo sapiens,

WO200177384-A2.

18-OCT-2001,

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DE-1019173

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 61536; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences. #X###X#X9999999999

Sequence 13 BP; 10 A; 0 C; 0 G; 3 T; 0 other;

Gaps ő Length 13; 0; Indels 1.0%; Score 13; DB 1; Le 100.0%; Pred. No. 3.1e+02; tive 0; Mismatches 0; Best Local Similarity 100.08 Matches 13; Conservative Query Match

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ABC61822 standard; DNA; 13 BP.

ABC61822;

21-FEB-2002 (first entry)

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Oligonucleotide SEQ ID NO 61839 for detecting SNP TSC0016434.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DB-1019173.

(BPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 61839; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,

ABC67270 standard; DNA; 13 BP.

RESULT 366

21-FEB-2002 (first entry)

ABC67270;

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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABP0010-ABR99889, ABH00010-ABR99989 and ABI00010-ABR82073 represent the oligomers described in the invention. WOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide SEQ ID NO 61840 for detecting SNP TSC0016434.
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                                                                                                                                                              Sequence 13 BP; 0 A; 0 C; 3 G; 10 T; 0 other;
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Best Local Similarity 100.0%; Pred. No. J..
Matches 13; Conservative 0; Mismatches
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ABC0010-ABS29989, ABF00010-ABF99989, ABH00010-ABH99989 and ABS10010-ABS2973 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the vipo.int/pub/published_pct_sequences.
                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                  Oligonucleotide SEQ ID NO 67287 for detecting SNP TSC0017611.
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100.0%; Pred. No. 3.1e+02;
ative 0; Mismatches 0;
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Query Match
1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The ABCOOND-ABKE9293 ABFOOND-ABF99999, ABHOOND-ABH99999 and ABFOOND-ABKE9999 ABFOOND-ABH99999 and ABFOOND-ABKE9999 and ABFOOND-ABKE9073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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             Oligonuclectide SEQ ID NO 67288 for detecting SNP TSC0017611
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Pred. No. 3.1e+02;
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100.0%; Pred. No. s...
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This invention describes novel oligomucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABC0010-ABG00
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100.0%; Pred. No. 3.1e+02;
ive 0; Mismatches 0;
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06-APR-2001; 2001WO-IB00713
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                                                 21-FEB-2002
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                                              ABC78656;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABF99989 and ABS00010-ABE89993 and SABO0010-ABE89993 and SABO0010-ABE89993 and SABO0010-ABE89999 and SABO0010-ABE99980 and SABO0010-ABE9980 and SABO0010-ABE99980 and SABO0010-ABE99980 and SABO0010-ABE9980 and SABO0010-ABE99980 and SABO0010-A
Claim 1; SEQ ID 72830; 29pp + Sequence Listing; German.
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ö Gaps ô 1.0%; Score 13; DB 1; Length 13; 00.0%; Pred. No. 3.1e+02; 0; Indels 100.08; Pred. ... Query Match Best Local Similarity 100.1 Matches 13; Conservative

ABC78656 standard; DNA; 13 BP

(first entry)

Oligonucleotide SEQ ID NO 78673 for detecting SNP TSC0020028.

SNP, single nucleotide polymorphism, human; diagnosis; PNA, cancer, CNS, peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

07-APR-2000; 2000DE-1019173

(RPIG-) RPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABD89989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formet from WIPO at ftp.wipo.int/pub/published_pot_sequences.

Claim 1; SEQ ID 78674; 29pp + Sequence Listing; German.

Claim 1; SEQ ID 78673; 29pp + Sequence Listing; German.

acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomers are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF9999, ABF00010-ABH99999 and ABI00010-ABH82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed This invention describes novel oligonuclectide primers or peptide nucleic

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Length 13;

1.0%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 3.18+02; ive 0; Mismatches 0; Indels

1134 TATAGTAAATTTA 1146

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13 ráragráaarrra 1

Local Similarity 100.

Matches

Query Match

Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 other;

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specification, but was obtained in electronic format from WIPO ftp.wipo.int/pub/published_pct_sequences.
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100.0%; Pred. No. 3.1e+02;
ative 0; Mismatches 0;
                                   Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 other;
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                                                         Query Match
Best Local Similarity
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                                                                             Matches
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ABC78657/0
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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                 Olek A, Piepenbrock C,
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                                Homo sapiens.
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                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                       Oligonucleotide SEQ ID NO 81459 for detecting SNP TSC0020625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.0%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 3,1e+02; ive 0; Mismatches 0; Indels
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                                              ABC81442 standard; DNA; 13 BP.
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                                                                                                                                                                                                                                                                                                                              (EPIG-) EPIGENOMICS AG
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                                                                                                21-PEB-2002
                                                                                                                                                                                                   Homo sapiens
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Matches
                    RESULT 372
ABC81442
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                                                                                                           set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status
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                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID 81460; 29pp + Sequence Listing; German.
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Local Similarity 100.0%; Pred. No. 3.1e+02;
tes 13; Conservative 0; Mismatches 0;
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Berlin K;
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06-APR-2001; 2001WO-IB00713. d ઠ

This invention describes novel oligonucleotide primers or peptide nucleic acid (FNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989 and ABB100101-ABE99989 and NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPPO at Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single nucleotide polymorphisms and cytosine methylation status Claim 1; SEQ ID 83569; 29pp + Sequence Listing; German ftp.wipo.int/pub/published_pct_sequences. Berlin K Olek A, Piepenbrock C, WPI; 2001-657177/75

Sequence 13 BP; 4 A; 0 C; 1 G; 8 T; 0 other;

Gaps .. 0 1.0%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 3.1e+02; tive 0; Mismatches 0; Indels Matches 13; Conservative Sest Local Similarity Query Match

1046 ATTIATGIATTIA 1058

ABC83553 standard; DNA; 13 BP ABC83553;

(first entry) 21-FEB-2002 Oligonucleotide SEQ ID NO 83570 for detecting SNP TSC0021049

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2

18-OCT-2001.

07-APR-2000; 2000DB-1019173

(EPIG-) EPIGENOMICS AG

Olek A, Piepenbrock C, WPI; 2001-657177/75

Berlin K;

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 83570; 29pp + Sequence Listing; German

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00110-ABC99989, ABF00010-ABH99989 and ABL00110-ABH99173 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences. 888888888888

Sequence 13 BP; 8 A; 1 C; 0 G; 4 T; 0 other;

ö Gaps ö Length 13; Query Match
1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels

1046 ATTIATGIATTIA 1058

Š gg RESULT 376 ABC83568

ABC83568 standard; DNA; 13 BP

ABC83568;

(first entry) 21-FEB-2002

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Oligonucleotide SEQ ID NO 83585 for detecting SNP TSC0021059.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DE-1019173

(BPIG-) EPIGENOMICS AG.

Berlin Olek A, Piepenbrock C,

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WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 83585; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABRE2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 3 A; 0 C; 1 G; 9 T; 0 other;

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 Length 13;
Score 13; DB 1; Length 13;
Pred. No. 3.1e+02;
0; Mismatches 0; Indels
                ilarity 100.0%; P
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                Best Local Similarity
Matches 13; Conserv
     Query Match
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ABC83569 standard; DNA; 13

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ABC83569;

21-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 83586 for detecting SNP TSC0021059.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DB-1019173

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 83586; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99889, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fig.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 9 A; 1 C; 0 G; 3 T; 0 other;

Gaps ö 1.0%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 3.1e+02; tive 0; Mismatches 0; Indels 13; Conservative Similarity Query Match Local

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RESULT 378

ABF01934 ID ABF01934 standard; DNA; 13 XX

(first entry) 21-FEB-2002

Oligonucleotide SEQ ID NO 101931 for detecting SNP TSC0025381.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; Es; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DB-1019173.

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 101931; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cycosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for disgnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The Oligoners are also used for detecting cell type differentiation. ABC0010-ABR182071 represent the oligomers described in the invention. MOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Sequence 13 BP; 2 A; 0 C; 3 G; 8 T; 0 other; ftp.wipo.int/pub/published_pot_sequences.

. 0 Length 13; 0; Indels 1.0%; Score 13; DB 1; Le 100.0%; Pred. No. 3.1e+02; 100.0%; Pred. no. Local Similarity 100. hes 13; Conservative Query Match Matches

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Gaps

1540 GATGITITIATGI 1552 1 GATGTTTTATGT 13 g ઠે

ABF01935 standard; DNA; 13 BP. ABF01935/

(first entry) 21-FEB-2002 ABF01935;

Oligonucleotide SEQ ID NO 101932 for detecting SNP TSC0025381.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 85; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001

Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, certical nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                06-APR-2001; 2001WO-IB00713.
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                                                                                     Claim 1; SEQ ID 112529; 29pp + Sequence Listing; German.
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ABC00010-ABC99389, ABF0010-ABF99989, ABH00010-ABH99989 and ABL00010-ABF99989, ABF99989, ABH0010-ABF99989 and system, cardiovascular and action the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in alectronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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ABC00010-ABC99989, ABF00010-ABF99989, ABH0010-ABH99989 and AB100010-ABH180731 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred. No. 3.1e+02;
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Best Local Similarity 100.0%; Pred. No. 3.1
Best Local Similarity 0; Mismatches
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABIS2973 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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100.0%; Pred. No. 3.16+02;
tive 0; Mismatches 0; Indels
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                              ABF15743 standard; DNA; 13
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Matches 13; Conservative
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1.0%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 3.1e+02; tive 0; Mismatches 0; Indels

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                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
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(RPIG-) EPIGENOMICS AG
                                              Piepenbrock
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABR80399, ABF0010-ABR99989 and ABR10010-ABR80373 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fip.wipo.int/pub/published_pct_sequences.
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Sequence 13 BP; 4 A; 0 C; 1 G; 8 T; 0 other;

Gaps ö 1.0%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 3.1e+02; ative 0; Mismatches 0; Indel8 Length 13; Best Local Similarity 100. Query Match

ò 셤 ABF20443 standard; DNA; 13 BP.

ABF20443;

(first entry)

21-FEB-2002

Oligonucleotide SEQ ID NO 120440 for detecting SNP TSC0030053.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-0CT-2001

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DE-1019173.

(EPIG-) EPIGENOMICS AG

Berlin Piepenbrock C, olek A,

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WPI; 2001-657177/75

Set of oligomucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 120440; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABP99989, ABH0010-ABH99989 and ABL00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed ftp.wipo.int/pub/published_pct_sequences.

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Matches 13; Conservative 0; Mismatches 0;
            Sequence 13 BP; 8 A; 1 C; 0 G; 4 T; 0 other;
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RESULT 388

ABF20500 standard; DNA; 13 BP.

ABF20500;

(first entry) 21-PSB-2002

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Oligonucleotide SEQ ID NO 120497 for detecting SNP TSC0030072.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2

18-0CT-2001.

06-APR-2001; 2001WO-IB00713.

(EPIG-) EPIGENOMICS AG

07-APR-2000; 2000DE-1019173

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 120497; 29pp + Sequence Listing, German.

This invention describes novel oligomucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and excessine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABR90999, ABR00010-ABR99989, ABH00010-ABR99989 and ABR00010-ABR99989 and ABR001010-ABR99989 and NOTE: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 5 A; 0 C; 0 G; 8 T; 0 other;

Gaps ö Length 13; Indels Query March
1.0%; Score 13; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0;

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1140 AAAITITATITAT 1152

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389 RESULT schultz143-3.rng

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                Set of oligonuclectides, useful for diagnosis and cell typing, idesigned to detect single nuclectide polymorphisms and cytosine methylation status
                                                                Oligonuclectide SEQ ID NO 120498 for detecting SNP TSC0030072
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This invention describes novel oligonucleotide primers or peptide mucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cancer also used for advovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0001D-ABE99899, ABH0001D-ABH99989 and ABC0001D-ABH99899 and ABG001D-ABH99989 and bashootle bashootle disperse described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fip.wipo.int/pub/published_pct_sequences. ö Gaps ö / Match 1.0%; Score 13; DB 1; Length 13; Local Similarity 100.0%; Pred. No. 3.1e+02; Nes 13; Conservative 0; Mismatches 0; Indels Query Match Best Loca Matches

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 133282 for detecting SNP TSC0033254.

ABF33285 standard; DNA; 13 BP

21-FEB-2002 (first entry)

ABF33285;

RESULT 390 ABF33284 ************

ABF33284 standard; DNA; 13 BP. ABF33284;

21-FEB-2002 (first entry)

Oligonuclectide SEQ ID NO 133281 for detecting SNP TSC0033254.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Berlin K;

Olek A, Piepenbrock C,

(BPIG-) EPIGENOMICS AG.

06-APR-2001; 2001WO-IB00713.

NO200177384-A2

18-OCT-2001.

Homo sapiens

07-APR-2000; 2000DE-1019173.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE09989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF9989, ABF00010-ABF9989 and should not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                   (RPIG-) EPIGENOMICS AG.
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                        WO200177384-A2
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                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABIS9399, ABF00010-ABF99999, ABH00010-ABH99999 and NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                 Claim 1; SEQ ID 133282; 29pp + Sequence Listing; German.
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.
ABC00010-ABC99989, ABP0010-ABE99989, ABH00010-ABE899989 and ABI00010-ABE82073 represent the oligomers described in the invention. OVER: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form at from WIPO at ftp.wipo.int/pub/published_pot_sequences.
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1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.18+02;
Matches 13; Conservative 0; Mismatches 0; Indels
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Best Local Similarity
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 153012 for detecting SNP TSC0038678.

21-FEB-2002 (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Mismatches
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nes 13; Conservative
13; Conservative
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Matches
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ABIF53104

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Set of oligomucleotides, useful for diagnosis and cell typing, i designed to detect single nucleotide polymorphisms and cytosine methylation status

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Piepenbrock C,

olek A,

WPI; 2001-657177/75.

(RPIG-) RPIGENOMICS AG

06-APR-2001; 2001WO-IB00713. 07-APR-2000; 2000DE-1019173

W0200177384-A2.

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Homo sapiens

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ABC00010-ABC99989, ABP00010-ABF99889, ABH00010-ABH99989 and ABI00010-ABR99989 and for detecting cell type differentiation.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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tive 0; Mismatches 0;
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ABF53015 standard; DNA; 13 BP

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1145 TATTTTATTTAG 1157

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Berlin

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABH0010-ABH99989 and ABB100110-ABE99989, ABH0010-ABH99989 and ABB10010-ABE9989, ABH0010-ABH99989 and be incential the oligomers as described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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100.0%; Pred. No. 3.1e+02;
rative 0; Mismatches 0;
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                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE199989, ABF00010-ABE199989 and ABI00010-ABE199031 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                             Length 13;
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                              Claim 1; SEQ ID 160864; 29pp + Sequence Listing; German.
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Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0;
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NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Matches 13; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
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                                                         Oligonucleotide SEQ ID NO 168615 for detecting SNP TSC0008285.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989 and ABS00010-ABE99989 and NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascullar and metabolic disorders. The Oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABF9989, represent the oligomers described in the invention. WOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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100.0%; Pred. No. 3.1e+02;
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(EPIG-) EPIGENOMICS AG.
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ABC10010-ABE29989, ABF00010-ABE9989 and ABE10010-ABE39989 and SABIO010-ABE9989 and SABIO010-ABE3073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Best Local Similarity 100.0
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ABF83258
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AC ABF8325
DT 22-FEB.
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Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 other; ftp.wipo.int/pub/published_pct_sequences.

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1.0%; Score 13; DB 1; Length 13;
100.0%; Pred. No. 3.1e+02;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.1e+02;
tive 0; Mismatches 0;
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     Query Match
Best Local Similarity 100.
Matches 13; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09999, ABF0010-ABE9999, ABH00010-ABH9999 and ABI00010-ABE9999, and the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status
                                                                                              Oligonucleotide SEQ ID NO 183899 for detecting SNP TSC0004785.
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                                                        22-FEB-2002 (first entry)
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                                                                                                                                                                                                                 Homo sapiens.
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                    ABP83902;
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0; Gaps
 Length 13;
                                   0; Indels
Match 1.0%; Score 13; DB 1; Le Local Similarity 100.0%; Pred. No. 3.1e+02; es 13; Conservative 0; Mismatches 0;
   Query Match
                                       Matches
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611 AATCTACAAAAA 623 13 AATCTACAAAA 1 ઠે

ABP83903 standard; DNA; 13 BP. 22-FEB-2002 (first entry) ABF83903;

Oligonucleotide SEQ ID NO 183900 for detecting SNP TSC0004785.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DE-1019173

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonuclectides, useful for diagnosis and cell typing, addesigned to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 183900; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosline methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for disquests and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC10010-ABR29989, ABR00010-ABR39999 and ABR10010-ABR39999 and NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 9 A; 2 C; 0 G; 2 T; 0 other;

Gaps ö 1.0%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 3.1e+02; ive 0; Mismatches 0; Indels Local Similarity 100. Les 13; Conservative Query Match Matches

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ABF88502 standard; DNA; 13 BP. RESULT 408 ABF88502

22-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 188499 for detecting SNP TSC0046423

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

-18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DB-1019173.

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligomucleotides, useful for diagnosis and cell typing, i designed to detect single mucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 188499; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF99989, ABH00010-ABF99989 and ABF00010-ABF98980 and ABF00010-ABF9980 and the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 other;

Gaps ö 1.0%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 3.1e+02; ative 0; Mismatches 0; Indels 13; Conservative Best Local Similarity Query Match Matches

1618 AAATATAATTTGT 1630 1 AAATATAATTTGT 13 ઠે

ABF88503 standard; DNA; 13 ABF88503;

BP.

(first entry) 22-FBB-2002

Oligonucleotide SEQ ID NO 188500 for detecting SNP TSC0046423.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo saptens.

WO200177384-A2.

18-OCT-2001

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DB-1019173

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 188500; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The

oligomers are also used for detecting cell type differentiation.
ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and
ABC100010-ABI82073 represent the oligomers described in the invention.
NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

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Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 other;

ö 1.0%; Score 13; DB 1; Length 13; 00.0%; Pred. No. 3.1e+02; 100.0%; Pred. ... Matches 13; Conservative Local Similarity Query Match

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Gaps

ð 셤 RESULT 410

BP. ABF94864 standard; DNA; 13

ABF94864;

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(first entry) 22-FBB-2002 Oligonucleotide SEQ ID NO 194861 for detecting SNP TSC0005457.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DE-1019173

(EPIG-) EPIGENOMICS AG.

Berlin K; Piepenbrock C, olek A,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 194861; 29pp + Sequence Listing; German.

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABR29389, ABF00010-ABR99989, ABR00010-ABH99989 and ABR00010-ABR99989, ABR00010-ABH99989 and shalloonle oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pot_sequences. ABP94864
XXX
ABP94864
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ABP9
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ABP9
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ABP9
AD 119

Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 other;

Gaps ö . Match 1.0%; Score 13; DB 1; Length 13; Local Similarity 100.0%; Pred. No. 3.1e+02; les 13; Conservative 0; Mismatches 0; Indels Query Match Best Local S Matches 13

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Oligonucleotide SEQ ID NO 213787 for detecting SNP TSC0052043.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                          Set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status
                                                                                                              Oligonucleotide SEQ ID NO 194862 for detecting SNP TSC0005457.
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                                                                                                                                                                                                                        06-APR-2001; 2001WO-IB00713
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TTTTAGATTAAA 1209
                                                           ABF94865 standard; DNA; 13
                                                                                                22-FEB-2002 (first entry)
          Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                      WO200177384-A2.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABIS2039 ABP0010-ABIS9989, ABH00010-ABH99989 and ABIC0010-ABIS2031 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fip.wipo.int/pub/published_pct_sequences. Claim 1; SEQ ID 194862; 29pp + Sequence Listing; German.

Gaps ö 1.0%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 3.1e+02; 7ative 0; Mismatches 0; Indels Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 other; Query Match Best Local Similarity 100.1 Matches 13, Conservative

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TTTTTAGATTAAA 1209
1197
                13
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ABH13810 standard; DNA; 13 (first entry) 22-FEB-2002 ABH13810; RESULT 412 ABH13810 ID ABH1 XX AC ABH1 XX DT 22-F XX

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cycosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABP99989, ABH00010-ABH99989 and ABIC0010-ABL82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fitp.wipo.int/pub/published_pct_sequences.
                          SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                     07-APR-2000; 2000DE-1019173.
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                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG
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                                                                                                                                                   WO200177384-A2.
                                                                                                                   Homo sapiens
                                                                                                                                                                                           18-OCT-2001.
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Gaps o; 0; Indels 1.0%; Score 13; DB 1; Le 100.0%; Pred. No. 3.1e+02; tive 0; Mismatches 0; Local Similarity 100. nes 13; Conservative Matches 8

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RESULT 413

ABH13811 standard; DNA; 13 BP

ABH13811/c

Oligonucleotide SEQ ID NO 213788 for detecting SNP TSC0052043. 22-FEB-2002 (first entry) ABH13811;

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

WO200177384-A2 Homo sapiens.

06-APR-2001; 2001WO-IB00713

Claim 1; SEQ ID 223125; 29pp + Sequence Listing; German.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single nucleotide polymorphisms and cytosine methylation status
                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide SEQ ID NO 223125 for detecting SNP TSC0054328.
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        07-APR-2000; 2000DE-1019173
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This invention describes more introductions between a solid (BNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABG00010-ABIS2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the wipo int/pub/published_pct_sequences. This invention describes novel oligonucleotide primers or peptide nucleic Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 other; Local Similarity 100.0%; Pred. No. 3... ies 13; Conservative 0; Mismatches ABH23149 standard; DNA; 13 BP. 1136 TAGTAAATTTATT 1148 1 TAGTAATTTATT 13 22-FEB-2002 (first entry) ABH23149; Query Match RESULT 415 ABH23149, % X S S S S S S S S S S S S X S ò 쉱 ö This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABIS99989, ABH00010-ABH99989 and ABI00010-ABIS9999, and celecting cell type differentiation. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences. Gaps oet or oligonuclectides, useful for diagnosis and cell typing, i designed to detect single nuclectide polymorphisms and cytosine methylation status ö Length 13; 1.0%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 3.1e+02; tive 0; Mismatches 0; Indels Claim 1; SEQ ID 213788; 29pp + Sequence Listing; German Sequence 13 BP; 8 A; 2 C; 0 G; 3 T; 0 other; Berlin K; Best Local Similarity 100. Matches 13, Conservative Piepenbrock C, (EPIG-) EPIGENOMICS AG. WPI; 2001-657177/75

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0; Indels

1.0%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 3.1e+02;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for disquests and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABH00010-ABE99989 and ABE00010-ABE99989, ABE00010-ABE9989 and NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide SEQ ID NO 223126 for detecting SNP TSC0054328.
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methylation status
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Berlin K;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The ABCOOUTO-ABCO9989, ABTOOUTO-ABCO9989, ABTOOUTO-ABCO9989, ABTOOUTO-ABCO9989 and ABIOOTO-ABCO9989 and ABIOOTO-ABCO9989 and ABIOOTO-ABCO9989 and ABIOOTO-ABCO9989 and Specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                            Oligonuclectide SEQ ID NO 227650 for detecting SNP TSC0055515
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                                 ABH27673 standard; DNA; 13
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                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                  Score 13; DB 1; Length 13;
Pred. No. 3.1e+02;
0; Mismatches 0; Indel8
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                                    Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 other;
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ftp.wipo.int/pub/published_pct_sequences.
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                                                                   Match 1.0%; Sc. Local Similarity 100.0%; P. R. es 13; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     designed to detect methylation status
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                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide SEQ ID NO 229373 for detecting SNP TSC00S5957.
                                   Length 13;
                                                                        0; Indels
                                 .Match
1.0%; Score 13; DB 1; Le
Local Similarity 100.0%; Pred. No. 3.1e+02;
les 13; Conservative 0; Mismatches 0;
Sequence 13 BP; 3 A; 2 C; 0 G; 8 T; 0 other;
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1587 TGGAAATATAAAA 1599

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Olek A, Piepenbrock C,
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                     WPI; 2001-657177/75
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methylation status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                      (RPIG-) EPIGENOMICS AG
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABC9989, ABF00010-ABH99899 and ABI00010-ABC99989, ABF00010-ABH99899 and Shinollo-ABC99989, ABF00010-ABH99989 and specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single nucleotide polymorphisms and cytosine methylation status
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100.0%; Pred. No. 3.1e+02;
tive 0; Mismatches 0; Indels
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Length 13;

1.0%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 3.1e+02; tive 0; Mismatches 0; Indels

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oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE099999, ABF00010-ABF99999, ABH00010-ABF99999 and ABI00010-ABF899999. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide SEQ ID NO 237842 for detecting SNP TSC0058010.
                                                                                                                          Sequence 13 BP; 2 A; 0 C; 4 G; 7 T; 0 other;
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nes 13; Conservative
                                                                                                                                                                                                                 GGGTTTTTAGATT 13
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                                                                                                                                                                                                                                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single nucleotide polymorphisms and cytosine methylation status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID 237842; 29pp + Sequence Listing; German.
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                                                                                                                                                             Berlin K,
07-APR-2000; 2000DE-1019173.
                                                                                                                                                             olek A, Piepenbrock C,
                                                                          (EPIG-) EPIGENOMICS AG
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Length 13;

1.0%; Score 13; DB 1;

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                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                            Oligonucleotide SEQ ID NO 248867 for detecting SNP TSC0060809.
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1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
100.0%; Pred. No. 3.1e+02;
ive 0; Mismatches 0; Indels
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ABH48891/C
ID ABH48891 standard; DNA; 13 BP.
AC ABH48891;
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     Best Local Similarity 100.
Matches 13; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNE) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE099989, ABH00010-ABH99989 and ABI00010-ABE09989, as oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in bectronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                  Oligonucleotide SEQ ID NO 248868 for detecting SNP TSC0060809.
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methylation status
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE09999, ABF00010-ABF99999, ABH00010-ABH99999 and ABE100010-ABE199999, acid for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pot_sequences.
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                                                                                      This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABP00010-ABH99999 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed typ.wipo.int/pub/published_pct_sequences.
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designed to detect single nucleotide polymorphisms and cytosine methylation status -
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and excessine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI0010-ABF3089, ABF00010-ABF99989, ABF00010-ABF99989 and ABI030010-ABF99989 and ABF99989 and ABI030010-ABF99989 and ABI030010-ABF99989 and ABI030010-ABF99989 and ABI030010-ABF99989 and ABI030010-ABF99989 and ABF99989 and ABF999899 and ABF99989 and A
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ABI00010-ABI82073 represent the oligomers described in the invention. NOTB: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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100.0%; Pred. No. 3.1e+02;
iive 0; Mismatches 0;
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                                                                                                                                            Sequence 13 BP; 8 A; 0 C; 2 G; 3 T; 0 other;
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Matches 13; Conservative
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABE99989, ABR00010-ABH99989 and ABI00010-ABE99899, ABR00010-ABH99989 and SABI00010-ABE9989, ABRO0010-ABH99989 and SABI00010-ABISQUAR for the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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100.0%; Pred. No. 3.1e+02;
tive 0; Mismatches 0;
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Matches 13; Conservative
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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single nucleotide polymorphisms and cytosine methylation status
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Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG. WPI; 2001-657177/75. designed to detect methylation status WO200177384-A2. 18-OCT-2001. 22-FBB-2002 ABH57674; Query Match Eca] 432 Best Loca Matches ABH57674 요 8 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABT89273 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fip.wipo.int/pub/published_pct_sequences. ö SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single nucleotide polymorphisms and cytosine methylation status ö Oligonucleotide SEQ ID NO 255536 for detecting SNP TSC0062287 Length 13; 0; Indels Claim 1; SEQ ID 255535; 29pp + Sequence Listing; German. Claim 1; SEQ ID 255536; 29pp + Sequence Listing; German. 1.0%; Score 13; DB 1; Le 100.0%; Pred. No. 3.1e+02; iive 0; Mismatches 0; Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 other; Berlin K; Berlin K; ABH55559 standard; DNA; 13 BP. 06-APR-2001; 2001WO-IB00713. 07-AFR-2000; 2000DE-1019173. 1427 ATATTAGTAATTT 1439 22-FEB-2002 (first entry) Local Similarity 100.0 1 Ararragrahrr 13 Olek A, Piepenbrock C, Piepenbrock C, (EPIG-) EPIGENOMICS AG (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75. WPI; 2001-657177/75 designed to detect methylation status WO200177384-A2. Homo sapiens. 18-OCT-2001. ABH55559; Query Match olek A,

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disconders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABC00010-ABC99989 and ABIO010-ABC99989, and cell type differentiation. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ttp.wipo.int/pub/published_pct_sequences.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cartioners are also system, cardiovascular and metabolic disorders. The ABCOOUIO-ABC9989, ABFOOUIO-ABH99989 and ABCOOIIO-ABC9989, ABFOOUIO-ABH99989 and ABCOOIIO-ABG9889, ABHOOIIO-ABH99989 and NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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designed to detect single nucleotide polymorphisms and cytosine
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                              Oligonucleotide SEQ ID NO 258389 for detecting SNP TSC0062829.
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ABH58412 standard; DNA; 13
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                                                                                                                                                                                                                                                                Oligonucleotide SEQ ID NO 257652 for detecting SNP TSC0062680
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Local Similarity 100.0%; Pred. No. 3.1e+02;
Hes 13; Conservative 0; Mismatches 0;
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1.0%; Score 13; DB 1; Le
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Matches 13; Conservative 0; Mismatches 0;
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Sequence 13 BP; 5 A; 0 C; 2 G; 6 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.0%; Score 13; DB 1; Length 13; 00.0%; Pred. No. 3.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID 258389; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 other;
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Best Local Similarity 100.0%; Fred. No. 3.1
Generative 0; Mismatchee
Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABH58413 standard; DNA; 13 BP.
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Piepenbrock C,
                                                                                                                   WPI; 2001-657177/75
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      olek A,
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LD ABHS 84.1
KX
AC ABHS 84.
KX
DT 22-FEB
XX
KW SNP; S
KW SPC CENT R
KW CH CH R
KW CH CH R
KW CH CH R
KW CH R
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0; Indels

1163 AAATGATGTTTTA 1175

Best Loca Matches

13 AAATGATGETTTA 1

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RESULT 434

ABH58412

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, artdiovascular and methololic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABMESQPS, ABF00010-ABMESQPS, ABF00010-ABMESQPS, and NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                       Set of oligomucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status
                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID 258390; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.0%; Score 13; DB 1; Le
Local Similarity 100.0%; Pred. No. 3.1e+02;
Nes 13; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                         06-APR-2001; 2001WO-IB00713.
                                                                                                                            07-APR-2000; 2000DE-1019173.
                                                                                                                                                                                                   Olek A, Piepenbrock C,
                                                                                                                                                                (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                   WPI; 2001-657177/75
               WO200177384-A2
                                                     18-OCT-2001
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Berlin

Oligonucleotide SEQ ID NO 262615 for detecting SNP TSC0009751. ABH62638 standard; DNA; 13 BP 1486 TATTATTAATG 1498 22-FEB-2002 (first entry) 13 TATTATTTAATG 1 ABH62638;

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.

WO200177384-A2. Homo sapiens

18-0CT-2001.

06-APR-2001; 2001WO-IB00713

07-APR-2000; 2000DE-1019173

(EPIG-) BPIGENOMICS AG.

Berlin K; Piepenbrock C, olek A,

WPI; 2001-657177/75

<u>1</u>8 Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 262615; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polyworphisms (SNP) and cytosine methylation status in chemically pretraated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABCO0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABCO0010-ABF9989, ABF00010-ABF99989 and ABCO0010-ABF9989, ABF00010-ABF9989 and ABCO0010-ABF9989, ABF00010-ABF9989, ABF00010-ABF99 **####X

Sequence 13 BP; 8 A; 0 C; 2 G; 3 T; 0 other;

Gaps ö Query Match
1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.18+02;
Matches 13; Conservative 0; Mismatches 0; Indels

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ABH62639 standard; DNA; 13 BP. 22-FEB-2002 (first entry) ABH62639; 437 ABH62639/

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Length 13; 0; Indels

Oligonucleotide SEQ ID NO 262616 for detecting SNP TSC0009751.

SNP, single nucleotide polymorphism, human; diagnosis; PNA, cancer, CNS, peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

06-APR-2001; 2001WO-IB00713. 18-OCT-2001.

07-APR-2000; 2000DB-1019173

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 262616; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytoshie methylation status in chemically pretreated genomic DNA. The aligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 266060 for detecting SNP TSC0064472

(first entry)

22-FBB-2002

ABH66083;

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ABH66083 standard; DNA; 13

RESULT 439 ABH66083

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.
ABC00010-ABC99389, ABF0010-ABH99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. ONTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                  Sequence 13 BP; 3 A; 2 C; 0 G; 8 T; 0 other;
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ABH66082 standard; DNA; 13 BP.
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Matches
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XXX ABH66

XXX ABH66

XXX ABH66

XXX SNP;

XXX SNP;

XXX BOD 18-0

XXX CENT 1
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Berlin K;

Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG

WPI; 2001-657177/75

06-APR-2001; 2001WO-IB00713. 07-APR-2000; 2000DE-1019173

WO200177384-A2. Homo Bapiens.

18-OCT-2001.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID 266060; 29pp + Sequence Listing; German.
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AAT56348
ID AAT56348 standard, RNA; 1:
XX
AC AAT56348;
XX
DT 25-MAR-2003 (updated)
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Length 13;

Query Match
1.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels

Sequence 13 BP; 8 A; 0 C; 1 G; 4 T; 0 other;

(first entry) 14-MAY-1997

Mouse TNF-a hammerhead ribozyme target sequence (nt position 1319). Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downegulation; interleukin-5; IL-5; ICA%-1; interceilular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; Translocation; chronic myelogenous leukaenia, CAL, cancer; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial inflammation; stroke; restenosis; ransplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawaeaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;

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resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit TNF-alpha expression, making them potentially useful for treating rheumatoid arthritis, septic shock and other inflammatory disorders including psoriasis, as well as for treatment of AlDS. (Updated on 25-MAR-2003 to correct PI field.)

Mus musculus.

AIDS; BB.

WO9523225-A2

95WO-IB00156 23-FEB-1995; 31-AUG-1995

95US-0380734

07-APR-1994;

9405-0201109.
9405-0218034.
9405-0218034.
9405-0224483.
9405-0228041.
9405-0245736.
9405-0291932.
9405-0291433.
9405-0391633.
9405-0311749.
9405-0311749.
9405-0311749.
9405-0311749.
9405-0318687. 16 MAX-1994 16-UUL-1994 16-AUG-1994 17-AUG-1994 17-AUG-1994 17-AUG-1994 19-AUG-1994 13-SEP-1994 13-SEP-1994 13-SEP-1994 13-SEP-1994 13-SEP-1994 13-SEP-1994 13-SEP-1994 13-SEP-1994 13-CCT-1994

94US-0363233

(RIBO-) RIBOZYME PHARM INC.

Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Grimm S, Karpelsky A, Kisich K, Matulic-adamic J, Mcswiggen JA; Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D; Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T:

WPI; 1995-351090/45.

Ribozymes having modified bases and methods for producing them for use in inhibiting disease related genes

Claim 2; Page 252; 407pp; English.

The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNP-alpha mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease

Gaps Enzymatic nucleic acid, ribozyme, trans cleavage, inhibition, gene expression, downregulation; interleukin-5; IL-5; ICMM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TWF-alpha, respiratory syncytial virus; RSV; bcr-abl; oncogene; TRF-alpha, respiratory syncytial virus; RSV; bcr-abl; oncogene; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arbthritis; psocriatis; myocardial ischaemia; Rawasati disease; septic shock; HTV; human immunodeficiency virus; acquired immune deficiency syndrome; Mouse TNF-a hammerhead ribozyme target sequence (nt position 1308) ö Query Match
1.0%; Score 13; DB 1; Length 15;
Best Local Similarity 30.8%; Pred. No. 3.5e+02;
Matches 4; Conservative 9; Mismatches 0; Indels Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other; AAT56318 standard; RNA; 15 BP. 950S-0380734.
940S-020109.
940S-022795.
940S-0227958.
940S-0227958.
940S-0227958.
940S-0217280.
940S-0211280.
940S-0211280.
940S-0303039.
940S-031486.
940S-031486.
940S-031486.
940S-031486.
940S-031486.
940S-031486.
940S-031486.
940S-031486. 1038 TATTTATTAT 1050 95WO-IB00156 25-MAR-2003 (updated) 14-MAY-1997 (first entry) 3 UAUTUAUTAUTA 15 Mus musculus. WO9523225-A2 16-AUG-1994; 17-AUG-1994; 19-AUG-1994; 23-FEB-1995; 31-AUG-1995. 10-NOV-1994; 23-SEP-1994; 28-SEP-1994; 15-APR-1994 15-AUG-1994 02-SEP-1994 08-SEP-1994 23-SEP-1994 07-0CT-1994 AAT56318; AIDS; BB. RESULT 441 888888

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Claim 2; Page 243; 407pp; English.
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                    9405-0201109
9405-0201109
9405-021834
9405-0228483
9405-0228481
9405-0228041
9405-02180
9405-02183
9405-0291433
9405-0291433
9405-0291433
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9405-0291433
9405-0291433
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94US-0316771.
94US-0319492.
94US-0321993.
94US-0334847.
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07-OCT-1994;
11-OCT-1994;
04-NOV-1994;
10-NOV-1994;
                                             04-APR-1994;
07-APR-1994;
15-APR-1994;
15-APR-1994;
18-MAY-1994;
06-JUL-1994;
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                                                                                                                         15-AUG-1994;
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19-AUG-1994;
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                                                          Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
Thompson JD, Tracz D, Usman N, Wincott FB, Woolf T;
                                                                                                                                                                                                              The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribbzzyme) which cleaves TNR-alpha mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA had do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit TNR-alpha expression, making them potentially useful for treating rheumatoid arthritis, septic shock and other inflammatory disorders including psoriasis, as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; rNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; rarablocation; chronic myelogenous leukeamia; CML; cancer; philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; rarangplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; CML swasaaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
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                                                                                                                                                  Ribozymes having modified bases and methods for producing them
for use in inhibiting disease related genes
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.0%; Score 13; DB 1; Length 15; Best Local Similarity 30.8%; Pred. No. 3.5e+02; Matches 4; Conservative 9; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 BP; 5 A; 0 C; 0 G; 10.U; 0 other;
                                                                                                                                                                                         Claim 2; Page 252; 407pp; English.
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94US-0357577.
94US-0363233.
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                                     (RIBO-) RIBOZYME PHARM INC.
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(first entry)
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                                                                                                                           WPI; 1995-351090/45.
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16-DEC-1994;
23-DEC-1994;
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25-MAR-1997
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Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, McGwiggen JA; Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D; Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a preferred target sequence for an enzymatic mucleic acid (i.e. a ribozyme) which cleaves TMP-alpha mRNA at the nucleotide base position indicated in the D3 line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit TMP-alpha expression, making them potentially useful for treating rheumatoid arthritis, septic shock and other inflammatory disorders including psoriasis, as well as
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Best Local Similarity 30.8%; Pred. No. 3.5e+02;
Matches 4; Conservative 9; Mismatches 0; Indels
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AAT55794
ID AAT5579
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AC AAT5579
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Human TNF-alpha hammerhead ribozyme target sequence (nt position 1256).
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                                                                             Enzymatic nucleic acid; ribozyme, trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; (ZMM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; TATANALOGATION; faront myed-logenous leukaemia; CML; cancer; philadelphia chromosome; inflammation; autoimmune disease; atherosolerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; poorlaals; myocardial ischemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 242; 407pp; English
                                                                                                                                                                                                                                                                                                                                                                                                              94US-0222795.
94US-0224483.
94US-0227958.
94US-0228041.
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94US-0271280.
94US-0291932.
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94US-0314397.
94US-0316771.
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94US-0311486
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94US-0218934
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             (updated)
(first entry)
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                                                                                                                                                                                                                                                         Homo sapiens.
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06-JUL-1994;
15-AUG-1994;
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28-SEP-1994;
03-OCT-1994;
07-OCT-1994;
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04-NOV-1994;
10-NOV-1994;
            25-MAR-2003
25-MAR-1997
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29-MAR-1994
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07-APR-1994
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                                                                                                                                                                                                                              AIDS; ss.
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Gaps
Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit TNF-alpha expression, making them potentially useful for treating rheumatoid architis, septic shock and other inflammatory disorders including psoriasis, as well as for treatment of AIDS.

(Updated on 25-WAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enzymatic nucleic acid, ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNP-alpha, respiratory syncytial virus; RSV; bor-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atheroselerosis; myocardial infarcation; stroke; restenosis; transplant rejection; rheumatoid architis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; whuman immunodeficiency virus; acquired immune deficiency syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSV N hammerhead ribozyme target sequence (nt. position 383).
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                                                                                                                                                                                                                              Sequence 15 BP; 5 A; 0 C; 0 G; 10 U; 0 other;
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94US-021109-94US-021109-94US-022795.
94US-0227958-94US-0227958-94US-0228041.
94US-0211280-94US-0291433-94US-0291437-94US-0303039-94US-03114397-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114337-94US-03114347-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03114437-94US-03144447
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(first entry)
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Best Local Similarity 30.07
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11-OCT-1994;
04-NOV-1994;
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15-MAR-1997
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17-AUG-1994
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Denton RR, Duda A, Nandabalan K,
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(SAIC-) SAICOM SRL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antitumcural phosphodiester oligonuclectide 15 with cytotoxic activity.
                                                                                                                                                                                            The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves mRNA coding for a protein of respiratory syncytial virus (RSV) at the nucleotide base position indicated in the DB line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the target sequences and can be used for treatment and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                     Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Stinm S, Karpelsky A, Kisich K, Matulic-adamic J, McBwiggen JA; Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D; Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
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                                                                                                                                             Ribozymes having modified bases and methods for producing them for use in inhibiting disease related genes
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Local Similarity 100.0%; Pred. No. 3.5e+02;
hes 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                              (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                   Sequence 15 BP; 7 A; 3 C; 1 G; 4 U; 0 other;
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                                                                                                                                                                            Claim 2; Page 274; 407pp; English.
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 94US-0337608.
94US-0345516.
94US-0357577.
94US-0363233.
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                                                   (RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                525 ATTTGAATTTCAG 537
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(first entry)
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                                                                                                                          WPI; 1995-351090/45.
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modified_base
 10-NOV-1994;
28-NOV-1994;
16-DEC-1994;
23-DEC-1994;
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24-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a'', b'', c'', d'', e'', f'', and g'' = 1-16, equal or different from each other;
                                                                                                                                                                                                                                                                                                                                      Novel phosphodiesteric oligonucleotides AAF93811-27 are based on the generic formula, in the 3'-5' or 5'-3' direction:

(GaTa')a'' - (GGTC')c'' - (GGTC')c'' - (GGTC')e'' - (GFTE')E'' - (GFTE')E'' - (GGTC')e'' - (GGTC')e'' - (GFTE')E'' - N and N' = T or G, equal or different from each other;

x = 0-8, equal or different from each other;
a, b, c, d, e, f, and g = 0-10, equal or different from each other;
a', b', c', d', e', f', and g' = 0-30, equal or different from each other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                               New phospho:di:esteric oligo:nucleotide(s) - which exert a specific and selective cytotoxic effect on tumour cells, for treating both solid and liquid tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, TNPRSF11B; osteoclastogenesis inhibitory factor; single nucleotide polymorphism; SNP; osteoclast recruitment; osteoclast function; osteoprosisis; metastatic bone disease; Paget's disease; rheumatoid arthritis; periodontal bone disease; ASO; allele-specific oligonucleotide; probe; ss.
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100.0%; Pred. No. 3.5e+02;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             particular lymphomas. (Updated on 25-MAR-2003 to correct PR field.)
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                                                                                                                                                                                                                                                                                  Claim 10; Page 6; 38pp; English.
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Quadrifoglio F, Scaggiante
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Best Local Similarity 100.(
Matches 13, Conservative
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The present sequence is a probe used to detect polymorphisms in the human osteoclastogenesis inhibitory factor (TWRSF11B). Polymuclectides comprising one or more of twenty four novel single mucleotide polymorphisms in the TWRSF11B gene have been identified. TWRSF1B regulate osteoclast recruitment and function. An understanding of variations in the gene should thus be useful in developing new therapies for metabolic disorders caused by abnormal osteoclast recruitment and function such as osteoporosis, metastatic bone disease, Paget's disease, rheumatoid arthritis and periodontal bone disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a probe used to detect polymorphisms in the human osteoclastogenesis inhibitory factor (TMFSRFIIB). Polymucleotides comprising one or more of twenty four novel single nucleotide polymorphisms in the TMFRSFIIB gene have been identified. TMFRSFIIB polymorphisms in the TMFRSFIIB gene have been identified. TMFRSFIIB variations osteoclast recruitment and function. An understanding of variations in the gene should thus be useful in developing new therapies for metabolic disorders caused by abnormal osteoclast recruitment and
        numman Usreoclastogenesis Inhibitory Factor nucleotides, comprising single nucleotide polymorphisms, useful for studying e.g. osteoporosis, Paget's disease and rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Osteoclastogenesis Inhibitory Factor nucleotides, comprising single nucleotide polymorphisms, useful for studying e.g. osteoporosis, Paget's disease and rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, TNPRSF11B, osteoclastogenesis inhibitory factor; single mucleotide polymorphism, SNP; osteoclast recruitment; osteoclast function; osteopiss; metastatic bone disease; Paget's disease; rheumatoid arthritis; periodontal bone disease; ASO; allele-specific oligonucleotide; probe; ss.
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Pred. No. 3.5e+02;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                    Sequence 15 BP; 4 A; 0 C; 1 G; 10 T; 0 other;
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                                                                                          Claim 15; Page 23; 114pp; English
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Best Local Similarity
Matches 13; Conserv
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Stephens JC;

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function such as osteoporosis, metastatic bone disease, Paget's disease, rheumatoid arthritis and periodontal bone disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                Gaps
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                                                                                                                                                                                                                                                                               ovarian cancer; ovarian disease; gene therapy; gene;
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                                                                                                                                                                                                                                                         Human ovary specific coding sequence SEQ ID NO: 27
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                                                        1.0%; Score 13; DB 1; Lv
100.0%; Pred. No. 3.5e+02;
ive 0; Mismatches 0;
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                                   Sequence 15 BP; 4 A; 0 C; 2 G; 9 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a coding sequence of the invention.
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                                                                                                       1147 TTTTATTTAGAT 1159
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(first entry)
                                                                                                                     TTTTATTTAGAT 13
                                                                                 13; Conservative
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Best Local Similarity
Matches 13; Conserv
                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                          WO200240720-A2.
                                                                                                                                                                                                                                                                                  Human; ovary;
cytostatic; ds
                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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19-NOV-1992
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                                                                        Local
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The present invention describes enzymatic nucleic acid molecules (NDMs) which specifically cleave RNA derived from an epidermal growth factor receptor (EGF-R) gene. AAV9721 to AAV984043 and AAV98979 to AAV99090 represent specifically claimed target sequence from human EGF-R. AAV98044 to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, epidermal growth factor receptor; EGFR; EGF-R; target sequence; hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation; cancer; genetic drift; detection; mutation; 88.
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                                                                                                                                              Claim 18 claims primers for use in detecting mutations in a mammalian gene for a structural protein of cartilage comprising a sequence identified in Table I (Page 18-31). Table I includes 179 primer sequences (see AAQ65728-Q65906). The following details are given for primer 86: Alt. code: DH-78
                                  Detecting genetic pre-disposition to osteoarthritis - and other diseases involving mutation in cartilage protein genes, by amplification and analysis of DNA and comparison with standards
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 17;
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100.0%; Pred. No. 3.9e+02;
vative 0; Mismatches 0;
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Primer position: 20135
(Updated on 25-MAR-2003 to correct FN field.)
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                                                                                                             Claim 18; Page 30; 112pp; English
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(UYAS-) UNIV ASTON.
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WPI; 1994-183530/22.
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                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JAN-1998;
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Prepn. of pro-UK comprises transforming a host cell with an expression vector contg. cDNA encoding pro-UK, derived from human vascular endothalial cells. The resultant transformant is cultured. The new type of pro-UK can be produced efficiently in large amts. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                         Efficient prodn. of pro-urokinase by genetic engineering -by transforming host cell by expression vector of deoxyribonucleic acid of human vascular endothelial cell, and culturing
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Ritvaniemi P, Williams CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Type II procollagen; COLZA1; amplification; primer; polymerase chain reaction; PCR; osteoarthritis; cartilage; ss.
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100.0%; Pred. No. 3.9e+02;
ive 0; Mismatches 0; Indels
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                                                      Prourokinase; vascular endothelial cell; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 8; 16pp; Japanese
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ID AAQ65895 standard; DNA; 17 BP.
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                                                                                                                                                                                                                                             90JP-0163144.
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              Pro-UK probe T6 (Td = 52).
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Best Local Similarity 100.
Matches 13; Conservative
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22-DEC-1994
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                                                                                         Synthetic
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AAV97736 Btandard; RNA; 17

AAV97736;

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hairpin ribozymes respectively for human EGF-R. The NAMs are useful for cleaving EGF-R RNA in the treatment of a condition associated with EGFR expression levels e.g. to inhibit cell proliferation in the prevention or treatment of cancers. The NAMs can also be used as diagnostic tools to examine genetic drift and mutantions within diseased cells or to detect the presence of EGF-R RNA in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, epidermal growth factor receptor; EGPR; EGF-R; target sequence; hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation; cancer; genetic drift; detection; mutation; ss.
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                                                                                                                                                              Length 17;
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1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 38.5%; Pred. No. 3.9e+02;
Matches 5; Conservative 8; Mismatches 0; Indels
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                                                                                                                           Sequence 17 BP; 2 A; 1 C; 4 G; 10 U; 0 other;
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97US-0036476.
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31-JAN-1997;
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                                                                                                                                                      Human, epidermal growth factor receptor; EGFR, EGP-R, target sequence, hammerhead ribozyme, hairpin ribozyme; inhibition; cell proliferation; cancer; genetic drift; detection; mutation; ss.
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                                                                                                                            Human BGF-R target sequence nucleotide position 4158.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Akhtar S, Fell P, McSwiggen JA;
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97US-0036476.
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Query Match
Best Local Similarity 38.5%,
Best Local Similarity 38.5%,
Aca 5; Conservative
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31-JAN-1997;
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AAV97737 standard; RNA; 17

AAV97737 RESULT 454
AAV97737
ID AAV9773
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Ouery Match 1.0%; Score 13; DB 1; Length 17; Best Local Similarity 38.5%; Pred. No. 3.9e+02; Matches 5; Conservative 8; Mismatches 0; Indels

McSwiggen JA;

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The present invention describes enzymatic nucleic acid molecules with RA cleaving activity, which specifically cleave RNA encoded by an aryl pydrocarbon nuclear transporter (ARNY) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17165 to AAA17622 represent ribozyme sequences for ARNY, corresponding target sequences; AAA17635 to AAA19185 to AAA19187 to AAA19185 to AAA21895 represent their corresponding target sequences; AAA19185 to AAA21861 and AAA21801 arget sequences; AAA21801 and AAA21801 and AAA21801 arget sequences; cfor integrin subunit beta 3, and AAA22476 to AAA23362, AAA23333 to the AAA21801 and AAA22201 and AAA22201 represent ribozyme sequence for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23333 to the ability of an mRNA encoding angiogenic factor, especially ARNT, are cepecially used to treat cancer, diabetic retinopathy, age related machine degeneration (ARND), inflammation, and arthritis, as well as angiofilbroma of tuberous sclerosis, pot wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber spatement in the levels of ARNT, Tie-2, integrin subunit alpha-1.
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integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
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                                                                                                                                                                                                                                                                                                                                                                      Pavco PA, Roberts B, Jarvis T,
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                                                                                                                                                                                                                                                                     27-MAR-1998;
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                                                             Homo sapiens.
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                                                                                                      Human, epidermal growth factor receptor; BGFR; BGF-R; target sequence; hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation; cancer; genetic drift; detection; mutation; ss.
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                                                               Juman BGF-R target sequence nucleotide position 4159.
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97US-0036476.
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Query Match Matches

ઠે 셤 Integrin subunit beta 3 substrate sequence SEQ ID NO:5914.

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The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl Nydcome, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAAA1555 to AAA1762 in a littegrin alpha 6 subunit gene, or a Tie-2 gene. AAAA1765 to AAA1765 to AAA186 to AAA2169 to
ophthalmologic; antiinflammatory; antiarthritic; antipeoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; vertaca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
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                                                                                                                                                                                 Homo sapiens
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The present invention describes enzymatic nucleic acid molecules with CC RNA clearing activity, which specifically cleave RNA encoded by an aryl Mydrocarbon nuclear transporter (ARNY) gene, an integrin submuit beta 3 gene, an integrin alpha 6 subwnit gene, or a Tie-2 gene. AAA16775 to AAA17167 and AAA17621 to AAA17622 represent ribozyme sequences for AAA196775 to AAA19154 represent ribozyme sequences for Tie-2, and AAA19087 to CC AAA19155 to AAA19152 represent their corresponding target sequences; AAA19155 to AAA19152 represent their corresponding target sequences; AAA19154 represent ribozyme sequences for Tie-2, and AAA19087 to AAA19155 to AAA19152 represent their corresponding target sequences; AAA19154 to AAA2168 represent their corresponding target sequences; CC AAA19253 to AAA21955 represent ribozyme sequences for integrin alpha 6 subminit, and AAA20362 to AAA21960 and AAA2196 to AAA2168 represent their corresponding target sequences; CC AAA21596 to AAA2168 represent their corresponding target sequences; CC AAA21596 to AAA2169 and AAA2342 and AAA22476 to AAA23342 represent ribozyme sequence for integrin submit beta 3, and AAA22476 to AAA23342. AAA23343 to AAA2342 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNY.

C stability of an mRNA encoding angiogenic factor, especially ARNY.

C stability of an degeneration (ARND), inflammation, psoriasis, verruca vulgaris, meovascular degeneration (ARND), inflammation, and arthritis, as well as angiofibroma of tubercosis, pot-wine stains, Sturge Webbr and other syndromes and diseases related to the levels of ARNT, Tie-2, integrin submit alpha-6, or integrin submit alpha-6, or integrin submit beta-3.
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                           Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; harmerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovaecular glaucoma; myopic degeneration; yerruca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Rippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; 88.
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ID AAA22689 standard; RNA; 17 BP.
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(first entry)

19-JUN-2000

AAA22689;

19-JUN-2000 (first entry)

Integrin subunit beta 3 substrate sequence SRQ ID NO:5915.

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; harmerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antidinflamatory; antiarthritic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; potrais; veruce vulgaris; angiofibroma; tuberous scierosis; potraine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens.

W09950403-A2

99MO-US06507. 24-MAR-1999;

98US-0079678 27-MAR-1998;

(RIBO-) RIBOZYME PHARM INC.

Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors

Claim 54; Page 236; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl wide cleaving activity, which specifically cleave RNA encoded by an aryl dydrocarbon nuclear transporter (ARNY) gene, an integrin subunit beeta 3 gene, and AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for AAA1767 to AAA17168 to AAA1768 to AAA1768 to AAA1768 to AAA1968 represent their corresponding target sequences; AAA19154 represent ribozyme sequences for Tie-2, and AAA19167 to AAA19155 to AAA19155 to AAA19155 to AAA1968 to AAA1968 to AAA1968 to AAA1968 to AAA1968 to AAA1967 to AAA19155 to AAA19155 to AAA1968 represent their corresponding target sequences; AAA19154 to AAA2168 represent their corresponding target sequences; AAA15950 to AAA2168 represent their corresponding target sequences; AAA15950 to AAA2168 represent their corresponding target sequences; AAA2159 to AAA2150 and AAA232363 to AAA23362 to AAA2333 to AAA23362 to AAA2333 to AAA2346 to AAA2334 to AAA2342 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an ENNA encoding angiogenic factor, especially ARNY, integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retiinopathy, age related macular degeneration (ARNO), inflammation, and arthritis as well as medicibroma of tubercous sclerosis, pot-wine stains, Sturge Weber syndrome, and other syndromes and diseases related to the levels of ARNI, Tie-2, integrin subunit alpha-6, or litegrin subunit alpha-6, or integrin subun

Sequence 17 BP; 4 A; 0 C; 1 G; 12 U; 0 other;

ö 1.0%; Score 13; DB 1; Length 17; 23.1%; Pred. No. 3.9e+02; ve 10; Mismatches 0; Indels Query Match Best Local Similarity 23.1%; Pred. No. 3.35 Conservative 10; Mismatches Query Match

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Gaps

1144 TTATTTTATTTA 1156 UNAUUUUAUUUUNA 14

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AAA22806 standard, RNA; 17 BP. RESULT 459 AAA22806/c

AAA22806;

(first entry) 19-JUN-2000

Integrin subunit beta 3 substrate sequence SEQ ID NO:6032.

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; anglogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; harmerhead ribozyme; anglogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; vertuca vulgaris; anglofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens.

409950403-A2

07-0CT-1999.

24-MAR-1999;

98US-0079678 27-MAR-1998;

(RIBO-) RIBOZYME PHARM INC.

Coeshott C, McSwiggen JA; Pavco PA, Roberts E, Jarvis T,

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors $\,$

Claim 54; Page 243; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl pydrocarbon nuclear transporter (ARNY) gene, an integrin submuit beta 3 gene, an integrin submuit beta 3 gene, an integrin submuit beta 3 gene, and AAA1761 to AAA1762 represent ribozyme sequences for ARNY; to AAA1765 to AAA1955 to AAA1955 to AAA1955 and AAA1835 and AAA19087 to Corresponding target sequences; and AAA1915 to AAA1952. represent their corresponding target sequences; and AAA1955 to AAA1952. represent their corresponding target sequences; AAA1952 to AAA21561 to AAA21559 represent ribozyme sequences; AAA1689 to AAA21561 and AAA21595 represent ribozyme sequences; AAA21689 to AAA21563 and AAA21595 represent ribozyme sequences for integrin alpha 6 subunit, and AAA2362 to AAA2334 to AAA2345 and AAA23476 to AAA23343 to AAA2345 to AAA2342 represent their corresponding target sequences; AAA2345 to AAA2345 and AAA23476 to AAA23343 to Corresponding target sequences for integrin subunit beta 3, and AAA22476 to AAA23362, AAA23343 to the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially asked to treat cancer, diabetic retinopathy, age related manual degeneration (ARW), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, and other syndrome, Kippel-Trenaumay-Weber sprace related to the syndrome, sud other syndromes and diseases related to the levels of ARW; Tie-2, and other syndromes and diseases related to the levels of ARW; Tie-2, and other syndromes and diseases related to the levels of ARW; Tie-2, integrin subunit alpha-6, or integrin subunit beta-3.

Sequence 17 BP; 0 A; 0 C; 3 G; 14 U; 0 other;

Query Match 1.0%; Score 13; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 3.9e+02;

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Indels

ő Mismatches ö 1208 AACAAACAAACAA 1220 Matches 13; Conservative ద ઢ

17 AACAAACAACAA 5 RESULT 46 AAA22811/

AAA22811;

AAA22811 standard, RNA; 17

19-JUN-2000 (first entry)

Human, aryl hydrocarbon nuclear transport, ARMT; TIB-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytocatatic; antidabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; nevascular glaucoma; myopic degeneration; periasis; veruca vulgaris; andiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Rippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss. Integrin subunit beta 3 substrate sequence SEQ ID NO:6037.

Homo sapiens

WO9950403-A2

37-0CT-1999.

99WO-US06507, 24-MAR-1999; 98US-007967B. 27-MAR-1998;

(RIBO-) RIBOZYME PHARM INC.

Jarvis T, Coeshott C, McSwiggen JA; Pavco PA, Roberts E, WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors

Claim 54; Page 244; 305pp; English

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl Nydrocarbon nuclear transporter (ARNY) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA1767 and AAA1765 to AAA1762 to AAA1767 and AAA1767 to AAA1955 to AAA1768 represent their corresponding target sequences; AAA1768 to AAA18185 and AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA19157 to AAA19155 to AAA19155 to AAA19155 to AAA19155 to AAA19157 to AAA19155 to AAA19155 to AAA19157 to AAA19157 to AAA19155 to AAA19157 to AAA19157 to AAA19157 to AAA19157 to AAA19157 to AAA19157 to AAA19159 to AAA1168 represent their corresponding target sequences; AAA15950 and AAA2159 to AAA21476 to AAA2352 to AAA2343 to AAA2159 to AAA2159 to AAA2343 to AAA2159 to AAA2159 to AAA2343 to AAA2342 represent their corresponding target sequences for integrin subunit beta 3, and AAA23476 to AAA233262, AAA2343 to AAA2342 represent their corresponding terget sequences.

Co AAA23422 represent their corresponding target sequences. The ribozyme sequence for integrin subunit beta 3, integrin subunit alpha-6, or Tie-2. They are stability of an mRNA encoding angiogenic factor, especially ARNY, age relaced to treat cancer, diabeter retinopathy, age relaced macular degeneration (ARNO), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, and other syndromes and diseases related to the levels of ARNI, Tie-2, integrin subunit alpha-6, or tie-2, where syndrome, other syndrome, other syndromes and diseases related to the levels of ARNI, Tie-2, integrin subunit alpha-6, or integrin subunit beta-3.

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Local Similarity 100.0%; Pred. No. 3.9e+02;
les 13; Conservative 0; Mismatches 0;
Sequence 17 BP; 1 A; 0 C; 5 G; 11 U; 0 other;
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1207 AAACAAACAAACA 1219

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AAV93569 standard; RNA; 17 BP.

AAV93569;

(first entry) 18-FEB-1999

Human B-raf substrate nucleotide position 1724.

Human, c-raf; A-raf; B-raf; hammerhead ribozyme, hairpin ribozyme, target; substrate; catalyst; modulation; expression; Raf gene; delivery; screaming; identification; synthesis; deprotection; purification; cancer; inflammation; psoriasts; non-hepatic ascites; infection; genetic drift; restenosis; rheumatoid arthritis; ss.

WO9850530-A2

12-NOV-1998

98WO-US09249 05-MAY-1998; 19-DEC-1997; 09-MAY-1997

09-JUL-1997;

970S-0068212. 970S-0046059. 970S-0049002. 970S-0056808. 970S-0061321. 970S-0061324. 22-AUG-1997; 02-OCT-1997; 02-OCT-1997; 05-NOV-1997;

(RIBO-) RIBOZYME PHARM INC

Beaudry A, Beigelman L, Bellon L, Burgin A, Jarvis T; Karpeisky A, Kisich K, Matulic-Adamic J, McSwiggen JA; Parry I, Reynolds M, Sweedler D, Thompson J, Workman CT;

WPI; 1999-009494/01.

Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, restenceis, and also new ribozymes and modified nucleoside triphosphates used as antiviral agents and synthons

Claim 177; Page 170; 259pp; English.

A method has been developed for the identification of a nucleic acid capable of modulating a process in a biological system. The method comprises: (a) introducing into the system a random library of nucleic acid catalysts (NAC) having a substrate binding domain (SBD), comprising a random sequence, and a catalytic domain (CD); and (D) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDs in such systems. Nucleic acid molecules with endonuclease activity and catalytic activity, from the present invention, are used to modulate gene expression in plant and mammalian invention, are used to modulate gene expression in plant and mammalian systemic diseases caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic ascites and infection. They may also be used to detect genetic drift and mutations in diseased cells and to determine RESULT 461

AAV93569

AAV93569

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AAV93569

DT 18-PBB

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KW Human,
KW Huma

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c-raf RNA. Specifically NACB with RNA-cleaving activity that modulate expression of the Raf gene, are used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of c-raf. Introduction of sugar/phosphate modifications increases atability against nuclease and activity. AAV99922 to AAV93877 represent NACS that can be used in the method, specifically for modulating the expression of a Raf gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    capable of modulating a process in a biological system. The method comprises: (a) introducing into the system a random library of nucleic acid catalysts (NAC) having a substrate binding domain (SBD), comprising a random sequence, and a catalytic dame in (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; c-raf, A-raf, B-raf, hammerhead ribozyme; hairpin ribozyme; target; substrate; catalyst; modulation; expression; Raf gene; delivery; screening; identification; synthesis; deprotection; purification; synthesis; approtection; purification; porciasis; non-hepatic ascites; infection; genetic drift; restenosis; rheumatoid arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, restenosis, and also new ribozymes and modified nucleoside
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, Kisich K, Matulic-Adamic J, McSwiggen JA;
eynolds M, Sweedler D, Thompson J, Workman
                                                                                                                                                                      1.0%; Score 13; DB 1; Length 17; 69.2%; Pred. No. 3.9e+02; tive 4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human B-raf substrate nucleotide position 1726.
                                                                                                                                       Seguence 17 BP; 6 A; 2 C; 3 G; 6 U; 0 other;
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97US-0046059.
97US-0051718.
97US-0056808.
97US-0061321.
97US-0064866.
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Parry T, Reynolds M,
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Matches 9; Conserv
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of at least part of the SBDs in such systems. Nucleic acid molecules invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic acidic RNA, e.g. cancer, inflammation, psoriasis, non-hepatic acidies and infection. They may also be used to detect genetic drift and mutations in diseased cells and to determine expression of the Raf gene, are used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of c-raf. Introduction of sugar/phosphate modifications increases stability against nuclease and activity, AAV90922 to AAV93877 represent NACs that can be used in the method, specifically for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, BR43/COUP-TF-1, the GATA transcription factor gene, TRP-2 and/or the CAATY Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha.
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                                                                                                                                                                                                                                              modulating the expression of a Raf gene.
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27-MAR-2001; 2001WO-US09761.
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100.0%; Pred. No. 3.9e+02;
cive 0; Mismatches 0; Indels
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Mismatches 0;
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100.0%; Pre-
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                Best Local Similarity 100.
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Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor. ZA; CDRVZA, melanoma; APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOB; mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein B; IULR; familial hypercholesterolaemia; UCII; syndrome; APP; BSBN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presentlin-1; Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor. BAR3/COUP-TR-1, the GATA transcription factor gene, IRR-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha.
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Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.
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100.0%; Pred. No. 3.9e+02;
tive 0; Mismatches 0;
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ABA78928 standard; DNA; 17
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hes 13; Conserv
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The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A (CDKN2A), APC, Pactor V, Pactor VIII, Pactor IX, haemoglobin alpha locus (CHRAI), haemoglobin alpha locus 2 (HBA2), Will, MSH2, MSH6, apolipoprotein B (APOB), LDL receptor (LDLR), UDP-glucuronosyltransferase (UGTI), amyloid precursor protein (APC), presentilin-1 (PSENI) and presentilin-2 (PSENI). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemoghilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia, harbelmer's disease, melanoma, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting oligonucleotides of the invention.
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                   27-MAR-2000; 2000US-192176P.
27-MAR-2000; 2000US-192179P.
01-UUN-2000; 2000US-208538P.
30-OCT-2000; 2000US-244989P.
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Length 17;
Match
Local Similarity 100.0%; Pred. No. 3.9e+02;
es 13; Conservative 0; Mismatches 0; Indels
                                                                     510 AAGAITCCIGGIT 522
      Query Match
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RESULT 467

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Homo sapiens

WO200173002-A2

04-OCT-2001

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ABA78929 standard; DNA; 17 BP. 24-JAN-2002 (first entry) ABA78929; ABA718929
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AC ABA7
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KW CCC
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Factor V mutation correcting oligonucleotide SEQ ID NO: 1775.

Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma, BRCA1; BRCA2, CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemoghilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE; mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein B; LDLR; familial hyperchlesterchaemia; UGT1; syndrome; APP; PSRN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1; Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;

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The present invention provides single-stranded oligomuclectides which can be used for the targeted alteration of genomic sequences, where the oligomuclectide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A (CDKN2A), APC, Pactor VIII, Factor IX, haemoglobin alpha locus (IMRA1), haemoglobin alpha locus 2 (HBA1), haemoglobin alpha locus 2 (HGT1), amyloid precursor protein (APC), presentilin-1 (FSRN3) and precursor protein (APC), presentilin-1 (FSRN3) and concer, adenosine deaminase deficiency, cystic fibrosis, such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia, Alzheimer's disease, melanoma, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting oligomucleotides of the invention.
                                                                                                                                                                                                                                                              Oligonuclectide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification -
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                                  27-MAR-2000; 2000US-192176P.
27-MAR-2000; 2000US-192179P.
01-JUN-2000; 2000US-208538P.
30-OCT-2000; 2000US-244989P.
27-MAR-2001; 2001WO-US09761.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAGATTCCTGGTT 13
                                                                                                                                                                              Gamper HB,
                                                                                                                                         (UYDE ) UNIV DELAWARE.
                                                                                                                                                                                                                       WPI; 2001-639230/73.
                                                                                                                                                                                Kmiec EB,
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ABA78932 standard; DNA; 17 BP. 24-JAN-2002 (first entry) ABA78932; RESULT 468 ABA 78932

Factor V mutation correcting oligonucleotide SEQ ID NO: 1778.

Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2, CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDKV2A; melanoma, APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VI; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE; mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein B; LDLA; familial hypercholesterolaemia; MGT1; syndrome; APP; FSEN1; antisense; UDP-qiucuromosyltransferase; amyloid precursor protein; presentilin-1; Althimer's disease; cytostatic; antisickling; antianaemic; haemostatic; antilipemic; sa

Homo sapiens.

#0200173002-A2.

04-OCT-2001

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The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch occapated with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, cretinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A (CDRX2), APC, Factor VIII, Pactor IX, haemoglobin alpha locus (CDRX2), APC, Pactor VIII, Pactor IX, haemoglobin alpha locus (CDRX1), mWA10, MSH6, MSH6, apolipoprotein B (APOB), LDL receptor (LDLR), UDP-glucuronosyltransferase (UGT1), amyloid precursor protein (APC), presentiln-2 (PSEX2). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemophilia, hypercholesterolaemia, thalassaemia, altche cell anaemia, larkelmer's diseases, melanoma, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting oligonucleotides of the invention.
                                                                                                                                                                                                                                                                                                 Oligonuclectide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification -
                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 149; 294pp; English.
                                                            27-MAR-2000; 2000US-192176P.
27-MAR-2000; 2000US-192199P.
01-JUN-2000; 2000US-208538P.
30-OCT-2000; 2000US-244989P.
                     27-MAR-2001; 2001WO-US09761
                                                                                                                                                                                                                  Kmiec EB, Gamper HB,
                                                                                                                                                                        (UYDE ) UNIV DELAWARE.
                                                                                                                                                                                                                                                            WPI; 2001-639230/73.
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ö Gapa ö 1.0%; Score 13; DB 1; Length 17; 100.0%; Pred. No. 3.9e+02; 0; Indels Sequence 17 BP; 8 A; 3 C; 3 G; 3 T; 0 other; Query Match
Best Local Similarity 100.0%; Fred. No. 3.9

510 AAGATTCCTGGTT 522 AAGAITCCTGGTT 4 16 셤

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ABA78933 standard; DNA; 17 BP. ABA78933; RESULT 469 ABA78933

(first entry) 24-JAN-2002

Pactor V mutation correcting oligonucleotide SEQ ID NO: 1779.

Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDRVA3; melanoma; APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOB; mismatch repair; MSH6; hyperlipideaemia; apolipoprotein B; LDHR; familial hypercholesterolaemia; UCFI; syndrome; APP; PSRNI; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presentiln-1; Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic; antilipemic; ss

Homo sapiens.

WO200173002-A2

27-MAR-2001; 2001WO-US09761. 04-OCT-2001

27-MAR-2000; 2000US-192176P. 27-MAR-2000; 2000US-192179P. 01-JUN-2000; 2000US-208538P. 30-OCT-2000; 2000US-244989P.

(UYDE) UNIV DELAWARE

Rice MC Gamper HB, Kmiec EB,

Rice MC

WPI; 2001-639230/73.

Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification -

Claim 7; Page 149; 294pp; English.

The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence are altered at each oligonucleotide has at least one mismatch compared with the genomic coligonucleotide at each oligonucleotide at denosine deanniase, p53, beta-globin, the following genes: adenosine deanniase, p53, beta-globin, corrective, practor V, Factor V, Factor VII, Factor IX, haemoglobin alpha locus C (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus C (UGYI), anyloid precursor protein (APC), presentlin-1 (PSEN1) and cuth as cancer, adenosine deaminase deficiency, cystic fibrosis, cuch as cancer, adenosine deaminase deficiency, cystic fibrosis, charmophilia, hypercholesterolaemia, thatassaemia, sictle cell anaemia, Alzheimer's disease, melanoma, adenomatous polyposis of the colon and cyatious syndromes. The present sequence is one of the gene correcting colons.

Sequence 17 BP; 3 A; 3 C; 3 G; 8 T; 0 other;

Gaps ö Length 17; 1.0%; Score 13; DB 1; Length 17; 100.0%; Pred. No. 3.9e+02; tive 0; Mismatches 0; Indels 13; Conservative Query Match Best Local Similarity Matches

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510 AAGATTCCTGGTT 522 AAGATTCCTGGTT 14 ਨੇ

ABK56156 standard; RNA; 17 RESULT 47

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ABK56156;

(first entry) 02-JUL-2002

Human CLCAl gene enzymatic nucleic acid #527.

Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antinflammatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic; acetylcysteine

Homo sapiens.

WO200211674-A2.

14-FEB-2002.

09-AUG-2001; 2001WO-US24970.

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                                                                                                                                                                                                                                                                                                   Bnzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma
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                                                                                                                                                                 McKenzie T, Ayers D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzymatic mucleic acid molecule of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 62; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK57482 standard; RNA; 17 BP
09-AUG-2000; 2000US-224383P
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                                                   (RIBO-) RIBOZYME PHARM INC (SYNT ) SYNTEX USA LLC.
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                                                                                                                                                              Thompson J, McSwiggen J, Grupe A,
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                                                                                                          (THOM/) THOMPSON J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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ID ABK574
XX AC ABK574
XX BY 02-JUL
XX BY Human,
XX Human,
XY AC ACCONT
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The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic thibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, caspociated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylycyteine and mucckinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and muttations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an
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                                                                                                                                                                                         Ensymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma
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                                                                         Szymkowski DE;
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                                                                         McKenzie T, Ayers D,
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                                                                                                                                                                                                                                                                                               Claim 4; Page 114; 152pp; English
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30-JAN-2001; 2001WO-US00662.
30-JAN-2001; 2001WO-US00663.
30-JAN-2001; 2001WO-US00664.
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                                                                         Thompson J, McSwiggen J,
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                                                                                                                                             WPI; 2002-217145/27
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                                                                                                     Grupe A;
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25-MAY-2001; 2001WO-US16981

06-DEC-2001

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                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of brotein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption of concentration, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in no particular heart and skeletal muscle disorders hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence.
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                                                                                                                                                                                                       Shannon ME
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                                                                                                                                                                                                                                                                                     New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 17;
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Local Similarity 100.0%; Pred. No. 3.9e+02;
les 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                       Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17 BP; 5 A; 6 C; 2 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID 7598; 214pp; English.
                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABN07612 standard; DNA; 17 BP.
30-JAN-2001; 2001W0-US00665.
30-JAN-2001; 2001W0-US00666.
30-JAN-2001; 2001W0-US00667.
30-JAN-2001; 2001W0-US00669.
30-JAN-2001; 2001W0-US00669.
30-JAN-2001; 2001W0-US00670.
                                                                                                                                                                                                                                                                                                                                                     myosin-like protein hGDMLP-l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s eccaccarctrac 17
                                                                                                                                                                                                           Ji Y, Penn SG,
                                                                                                                                                                                                                                                  WPI; 2002-179446/23.
                                                                                                                                                                    (AEOM-) AEOMICA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABN07612;
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                                                                                                                                                                                                           Gu Υ,
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WO200192524-A2 Homo sapiens

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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polymucleotide sequences of protein 1 (hGDMLP-1). The protein and polymucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 mucleic acids in samples, as amplification and quantify hGDMLP-1 uncleic acids in samples, as amplification or confidents, to provide initial substrates for the recombinant engineering or confunction to provide initial substrates for the recombinant engineering of hGDMLP-1 proteins. The hGDMLP-1 proteins or polymeptides may be used as immunogens to raise antibodies that specifically recognise concentration and/or amount specifically of hGDMLP proteins, as specific concentration, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polymucleotide sequences encoding hGDMLP-1 may be used for therapy. The polymucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in continue to chromosome 22. The present sequence represents an oligomer used in the increase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shannon ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein bGDMLP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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100.0%; Pred. No. 3.9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 4 A; 6 C; 2 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID 7604; 214pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gu Y, Ji Y, Perm SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK17633/c
ID ABK17633 standard; RNA; 17 BP.
XX
                           2001WO-US00661.
2001WO-US00662.
2001WO-US00663.
                                                                                                                      30-JAN-2001; 2001MO-US00664.
30-JAN-2001; 2001MO-US00665.
30-JAN-2001; 2001MO-US00666.
30-JAN-2001; 2001MO-US00667.
                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00668.
                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00670
                                                                                                                                                                                                                                                                                                                                                             05-PEB-2001, 2001US-266860P
2000GB-0024263
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Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-179446/23.
                                                                                                                                                                                                                                                                                                                                                                                                                            (ABOM-) AEOMICA INC.
04-OCT-2000;
                                                                     30-JAN-2001;
                                                                                              30-JAN-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nvention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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ABK17633;

09-APR-2002 (first entry)

Human ERG hammerhead ribozyme target sequence, Seq ID No 280.

Human; harmerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port.wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme; amberzyme.

domo sapiens.

WO200188124-A2.

22-NOV-2001.

16-MAY-2001; 2001WO-US15866.

16-MAY-2000; 2000US-0572021.

(RIBO-) RIBOZYMB PHARM INC. (GLAX) GLAXO GROUP LID.

Jarvis T, Von Carlowitz I, McSwiggen JA, Mclaughlin F, Randi AM;

WPI; 2002-082995/11.

Novel polynucleotide which down regulates expression of Ets-related gene, useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome

Claim 4; Page 63; 149pp; English.

The invention relates to a nucleic acid molecule (I) which down regulates conditions selected from cancer, lymphoma, Ewing's sacroma, malanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, tumour angiogenesis, diabetic retinopathy, macular degeneration, tumour angiogenesis, diabetic retinopathy, macular degeneration, cumour angiofibroma of tuberous sclerosis, port-wine stains, Sturge Weber syndrome, leukaemia, osteoprosis and wound healing. (I) is useful for syndrome, leukaemia, osteoprosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies under conditions suitable for the treatment. Leukaemia or tumour conjunction with one or more of contacting (I) to the patient in conjunction with one or more of officer therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting (I) with RNA, in the presence of a divalent cation such as Mg2+. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically cation genes. ABK17354-ABK22719 represent nucleic acide, including antisense and catacher present nucleic acide, including antisense and catacher present nucleic acide, including antisense considered by and catacher within regulate expression of ERG, and catacher presents of the invention.

Sequence 17 BP; 7 A; 1 C; 2 G; 7 U; 0 other;

Gaps ö Length 17; 1.0%; Score 13; DB 1; Length 17; Similarity 100.0%; Pred. No. 3.9e+02; 13; Conservative 0; Mismatches 0; Indels 13; Query Match Best Local & Matches

14 ATTTTABATACA 2

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RESULT 475

ABT34689 standard; DNA; 17

ВÞ.

ABT34689;

(first entry) 12-JUN-2003 rumour suppression related human fukutin oligo SEQ ID No 326.

Cytostatic, virucide, neuroprotective, nootropic, neuroleptic, gene chip, antisense, sense, tumour, cell degeneration, cancer; Alzheimer's disease, edizophrenia; protein chip, gene therapy, tumour suppression, human fukutin, ds.

WO2003025175-A2.

27-MAR-2003.

17-SEP-2002; 2002WO-IB04208.

17-SEP-2001; 2001FR-0011978.

(MOLE-) MOLECULAR ENGINES LAB.

Tuijnder M; relerman A, Amson R,

PPI; 2003-313353/30.

New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells

Disclosure; Page 72; 720pp; French.

The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive mucleotides from the 17 mer sequence, a sequence, a sequence at least 80 k identity to the 17 mer sequence, a sequence at least 80 k identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding NNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for disagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and chops. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression related human fukutin oligonucleotide of the invention.

Sequence 17 BP; 7 A; 1 C; 5 G; 4 T; 0 other;

ö 1.0%; Score 13; DB 1; Length 17; 100.0%; Pred. No. 3.9e+02; tive 0; Mismatches 0; Indels 13; Conservative Best Local Similarity Query Match Matches

Gabe

419 ATCAGTGAAGATG 431

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ATCAGTGAAGATG 14

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The invention relates to the isolation of the Arabidopsis thaliana MSH3 (AAX79066) and MSH6 (AAX79067) genes. These genes are MutS homologues (MSH) from plants and are involved in DNA mismatch repair. The DNA sequence can be used in processes for at least partially inactivating a DNA mismatch repair system of a plant, for increasing genetic variation in a plant, and for obtaining a plant with a desired characteristic. Printers AAX79105-X79160 represent 28 primer pairs used to amplify short allelic repeat fragments designated Simple Sequence Length Polymorphisms (SSLP). These fragments can be used as markers in the analysis of homologous recombination between genomes of A.thaliana subspecies.
                                                                                                                                                    MSH6; MutS homologue; plant; DNA mismatch repair; genetic variation; characteristic; microsatellite; primer; PCR; amplification; SSLP; ss; simple sequence length polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding protein functionally involved in the DNA mismatch repair system of a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 1.0%; Score 13; DB 1; Length 18; Local Similarity 100.0%; Pred. No. 4.1e+02; nes 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Perez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 BP; 8 A; 5 C; 5 G; 0 U; 0 other;
                                                                                                                           Primer NGA63-F for A.thaliana SSLP marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                Betzner AS, Doutriaux M, Freyssinet G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sxample 3; Page 26; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  (RHON ) RHONE-POULENC AGROCHIMIE
                                AAX79107 standard; DNA; 18 BP.
                                                                                                                                                                                                                                                                                                                                       98WO-EP06977
                                                                                                                                                                                                                                                                                                                                                                   97AU-0009745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                895 CTGTGCCTTGGTT 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGTGCCTTGGTT 1
                                                                                            (first entry)
                                                                                                                                                                                                                      Synthetic.
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-277644/23.
                                                                                                                                                                                                                                                                                                                                       09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                     10-0CT-1997;
                                                                                            17-AUG-1999
                                                                                                                                                                                                                                                                     WO9919492-A2
                                                                                                                                                                                                                                                                                                     22-APR-1999
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                                                            AAX79107,
Matchea
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The present invention describes a transcription factor regulating the expression of ethylene-inducible genes in plants, having DNA binding activity specific to the consensus sequence A(T/C)(GA/T)A(C/T) CT. The present invention describes the tobacco ethylene insensitive 3 (BIN3)-like protein, designated TELL, isolated from Nicotiana tabacum cv Samsun NN. The transcription factor is used to impart environmental stress resistence to plants by transformation with the gene for the transcription factor, and screening potential inhibitors of the expression of ethylene-inducible genes in plants. AAZ95383 to AAZ95476 represent oligonucleotides used in the exemplification of the present

Sequence 18 BP; 6 A; 4 C; 4 G; 4 T; 0 other;

Transcription factor regulating the expression of ethylene-inducible genes and gene encoding it, useful for imparting resistance to environmental stress to plants

Example 3; Fig 5; 65pp; Japanese.

(NORQ) NAT INST AGROBIOLOGICAL RESOURCES MIN. (NISC-) JAPAN SCI & TECHNOLOGY CORP.

Ohashi Y, Kosugi S; WPI; 2000-206011/18.

99WO-JP02347.

06-MAY-1999;

24-FEB-2000

Nicotiana tabacum.

C - T 7 T T T T 7 S

TITO DEC TO 01:73:70 7003

WO200009712-A1.

98JP-0227448

11-AUG-1998;

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ö
                                                                                                                                                                                                    Messenger ribonucleic acid; mRNA binding motif; immunogen; cell growth; Grb7; epidermal growth factor receptor; RGF-R; REWSA; ss.
                       Gaps
                      ;
0
1.0%; Score 13; DB 1; Length 18;
100.0%; Pred. No. 4.1e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                  EGF-R mRNA specific oligomer EGF-23a.s.
                                                                                                                                                                                                                                                                                                                                                                  Thomson A;
                                                                                                                                                                                                                                                                                                                                               (UYWA-) UNIV WESTERN AUSTRALIA.
                                                                                                                     AAH22863 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                          99AU-0004835.
                                                                                                                                                                                                                                                                                                     22-DEC-2000; 2000WO-AU01595
                                             SSS TICATIGIACCAT 567
                                                                                                                                                               (first entry)
  Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                       13 TTCATTGTACCAT 1
                                                                                                                                                                                                                                                                                                                                                                   Balmer L,
                                                                                                                                                                                                                                                            WO200148193-A1
                                                                                                                                                                                                                                                                                                                          23-DEC-1999;
                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                   Leedman PJ,
                                                                                                                                          AAH22863;
                                                                                                  RESULT 478
                                                                                                              AAH22863
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Tobacco, ethylene insensitive 3; TEIL; transcription factor; plant; regulation; ethylene inducible gene; environmental stress; resistance; ss.

TEIL random binding site selection oligonucleotide #73

(first entry)

01-JUN-2000

AAZ95455

AAZ95455 standard; cDNA; 18 BP.

RESULT 477

WPI; 2001-418275/44.

The invention provides an messenger ribonucleic acid (mRNA) binding motif that is capable of binding and destabilising the mRNA. The mRNA binding motif is useful as an immunogen to generate antibodies, which are useful as standards in assays for the motif ligand, for detecting the motif ligand in clinical samples for diagnostic purposes, and for in vivo imaging. A polypeptide that is specifically co-precipitated by the artibody is useful for effecting a number of interventions into cell growth and proliferation. Sequences AAR22857-66 represent sense and antisense DNA oligomers specific for epidermal growth factor receptor (EGF-R), used in RNA electrophoretic gel mobility shift assay (REMSA). Novel mRNA binding motif that is capable of binding and destabilizing the mRNA, useful as an immunogen to generate anti-mRNA binding motif antibodies which are useful for diagnostic purposes Example 1; Fig 3; 87pp; English.

Sequence 18 BP; 2 A; 3 C; 5 G; 8 T; 0 other;

Gaps ç, Length 18; 0; Indels 1.0%; Score 13; DB 1; Le 100.0%; Pred. No. 4.1e+02; trive 0; Mismatches 0; Query Match
Best Local Similarity 100.
Matches 13; Conservative

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셤 8

RESULT 479

AAH22864 standard; DNA; 18

B

AAH22864;

07-SEP-2001 (first entry)

EGF-R mRNA specific oligomer BGF-23a.as.

Messenger ribonucleic acid; mRNA binding motif; immunogen; cell growth; Grb7; epidermal growth factor receptor; EGF-R; REMSA; ss.

Homo sapiens

WO200148193-A1.

05-JUL-2001

22-DEC-2000; 2000WO-AU01595.

99AU-0004835. 23-DEC-1999; (UYWA-) UNIV WESTERN AUSTRALIA

Thomson A; Leedman PJ, Balmer L,

WPI; 2001-418275/44.

Novel mRNA binding motif that is capable of binding and destabilizing the mRNA, useful as an immunogen to generate anti-mRNA binding motif antibodies which are useful for diagnostic purposes

Example 1; Fig 3; 87pp; English.

The invention provides an messenger ribonucleic acid (mRNA) binding motif that is capable of binding and destabilising the mRNA. The mRNA binding motif is useful as an immunogen to generate antibodies, which are useful as standards in assays for the motif ligand, for detecting the motif ligand in clinical samples for diagnostic purposes, and for in vivo imaging. A polypeptide that is specifically co-precipitated by the antibody is useful for effecting a number of interventions into cell AAH22864/
XX AAH22
XXX AAH

ö growth and proliferation. Sequences AAH22857-66 represent sense and antisense DNA oligomers specific for epidermal growth factor receptor (SGF-R), used in RNA electrophoretic gel mobility shift assay (REMSA) Gaps ö Length 18; 0; Indels 1.0%; Score 13; DB 1; Le 100.0%; Pred. No. 4.1e+02; tive 0; Mismatches 0; Sequence 18 BP; 8 A; 5 C; 3 G; 2 T; 0 other; 550 AGTTTTTCATTGT 562 Local Similarity 100. 16 AGTTTTTCATTGT 4 Query Match Matches 888888 88888 셤

RESULT

AAF89440 standard; DNA; 18 BP.

14-AUG-2001 (first entry) AAF89440;

Human genetic marker PCR primer SEQ ID NO: 29,

Genetic marker; genetic disease diagnosis; cystic fibrosis; haemophilia; sickle cell disease; muscular dystrophy; Huntington's disease; retinoblastoma; PCR primer; ss.

Homo sapiens

WO200134839-A1,

17-MAY-2001.

03-NOV-2000; 2000WO-US30493

99US-0165301. 12-NOV-1999;

(DUNL/) DUNLOP C L M. (WEIS/) WEISEL J M.

Dunlop CLM, Weisel JM;

WPI; 2001-329096/34.

Detecting multiple genetic markers in one assay, useful to simultaneously detect a number of genetic disorders, comprises generating extension products and separating them on the basis of melting behavior is

Claim 44; Page 33; 40pp; English.

The present invention describes a method of inentifying the presence of a plurality of genetic markers in a subject, involving generating extension products using PCR primers flanking the plurality of markers, separating the extension products depending on their melting temperatures, and analysing them to determine the presence or absence of each genetic marker. This can be used in the diagnosis of genetic diseases, including familial hypercholesterolaemia, cystic fibrosis, Tay-Sachs, thalassaemia, sickle cell disease, phenylketomuria, galactosis, Tay-Sachs, thalassaemia, sickle cell disease, phenylketomuria, galactosis, dehydrogenase, maturity onset diabetes, cystinuria, methylmolonic acidaemia, urea cycle disorders, hereditary fructose intolerance, hereditary haemochromatosis, neonatal thrombocytopenia, daucher's disease, tyrosinaemia, urea cycle disorders, adenomia, adult polycystic kidney disease, radininaemia, shutingon's disease, adult polycystic kidney disease, tolorectal cancer, Huntington's disease, adult polycystic kidney disease, retinoblastoma, syndrome, neurofibromatosis, osteogenesis imperfecta, retinoblastoma, reuropathy, MCAD, Canavan's disease, retinitis pigmentosa, Bloom syndrome, Panconi anaemia or Neimann Pick disease. The present sequence AAR89440/C
AAR89440/C
AAR89440/C
AAC846
AAC AAR89
AAC AAR89
AAC AAR89
AAC AAR89
AAC AAR80
AAC AAR80
AAC AAR80
AAC AAR80
AAC AAR80
AAC AAR80
AAC AAC80
AAC AA

Query Match

SXS

Best Loca Matches

AAF87476;

RESULT 481 AAF87476

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Shrimp; heat labile alkaline phosphatase; SAP; DNA sequencing reaction; cloning vector dephosphorylation; PCR amplification product-mixture; reporter enzyme; PCR; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is provided in a specification relating to ge encoding thermophilic amino acid biosynthesis system enzymes of the thermortolerant bacterium Corrubbacterium thermoaminogenes. The novel proteins retain at least 30% isocitrate ligase activity after heating at 500C for 5 minutes. DNA fragments encoding the carymes were isoclated from a Corrubbacterium thermoaminogenes chromosomal DNA plasmid library by FOR. The DNA may be used for developing strains of amino acid producing microorganisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteins and their DNA useful for microbial production of L-amino
                                                                                                                                                               Corynebacterium, thermophilic, amino acid biosynthesis, enzyme, thermotolerant, acea, accBC, dtsRl, dtsR2, pfk, scrB; gluABCD; pdhA, pc; ppc; acn; icd, lpd; odhA; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hirano S, Nonaka G, Matsuzaki Y, Akiyoshi N, Nakamura K, Osumi T, Matsui K, Kawahara Y, Kurahashi O, Nakamatsu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.0%; Score 13; DB 1; Length 18;
100.0%; Pred. No. 4.1e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                 Corynebacterium thermoaminogenes icd primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 28; 215pp; Japanese.
                                                                                                                                                                                                                                                   Corynebacterium thermoaminogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВР.
AAF87482/c
ID AAF87482 standard; DNA; 18 BP.
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01-NOV-1999; 99JP-0311147.
21-APR-2000; 2000JP-0120687.
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                                                                                               (first entry)
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Best Local Similarity 100.
Matches 13, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AJIN ) AJINOMOTO CO INC.
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                                                                                               09-JUL-2001
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                                                         AAF87482;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hirano S, Nonaka G, Mateuzaki Y, Akiyoshi N, Nakamura K, Kimura B;
Osumi T, Matsui K, Kawahara Y, Kurahashi O, Nakamatsu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteins and their DNA useful for microbial production of L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is provided in a specification relating to genes encoding thermophilic amino acid biosynthesis system enzymes of the thermotolerant bacterium Corynebacterium thermoaminogenes. The novel proteins retain at least 30% isocitrate ligase activity after heating at 500C for 5 minutes. DNA fragments encoding the enzymes were isolated from a Corynebacterium thermoaminogenes chromosomal DNA plasmid library by PCR. The DNA may be used for developing strains of amino acid producing microorganisms
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                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium; thermophilic; amino acid biosynthesis; enzyme; thermotolerant; aceA; aceBC; dteRl; dteR2; pfk; scrB; gluABCD; pdhA; pc; ppc; acn; icd; lpd; odhA; PCR primer; ss.
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                                                                            . Match 1.0%; Score 13; DB 1; Length 18; Local Similarity 100.0%; Pred. No. 4.1e+02; es 13; Conservative 0; Mismatches 0; Indels
                                                                                Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium thermoaminogenes icd primer.
                                          Sequence 18 BP; 5 A; 2 C; 6 G; 5 T; 0 other;
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    is one of the PCR primers of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium thermoaminogenes
                                                                                                                                                                                                                                                                                                    AAF87476 standard; DNA; 18 BP.
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01-NOV-1999; 99JP-0311147.
21-APR-2000; 2000JP-0120687.
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                                                                                                                                                            799 TGCCATAAAGTCA 811
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Les 13, Conservative
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Query Match

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RESULT 482

21-PBB-2002.

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Microbial virulence factor; genetic predisposition, Alzheimer's disease; Parkinson's disease; schizophrenia; frontotemporal lobe dementia; hereditary wulti-infarct dementia; primary X-linked mental retardation; dementia; myopathy; familial British dementia; psychiatric disorder; transgenic animal; amyloid precursor protein; APP; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of shrimp (Pandalus borealis) heat labile alkaline phosphatase (B.C. 3.1.3.1) referred to as SAP, and polymucleotide sequences encoding it. The SAP enzyme is useful in the dephosphorylation of cloning vectors prior to ligation reactions, in the breatment of PCR amplification product-mixtures prior to DNA sequencing reactions, in molecular biology techniques, in the production of DNA based therapeutics or in forensic science, for laboratory protocols, and as a reporter enzyme. The SAP enzyme is heat labile and cold active making it particularly suitable for use in multi-steep laboratory protocols where a simple heating step deactivates the enzyme. The present sequence represents a SAP PCR primer used in the examples of the
                                                                                                                                                                                                                                                                                                                                                                       Novel recombinant heat labile shrimp alkaline phosphatase useful in molecular biology techniques, in the production of DNA based therapeutics or in forensic science, and for laboratory protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella typhimurium amyloid precursor protein (APP) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.0%; Score 13; DB 1; Length 18; 72.2%; Pred. No. 4.1e+02; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                    (NOFI-) NORWEGIAN INST FISHERIES & AQUACULTURE.
(GARD/) GARDNER R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 7 A; 1 C; 4 G; 2 T; 4 other;
                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 34; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               886 CTTGTTCCACTGTGCCTT 903
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/mod_base= i
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Best Local Similarity 72.2
Matches 13, Conservative
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                                                                                                                                                                                                                                                                                                         Sardner R, Nilsen I,
                                                                                                                                                                                                                                                                                                                                          WPI; 2002-444182/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention.
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                                                                                                                    VO200231157-A2
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modified_base
                                                                                                                                                     18-APR-2002
Synthetic
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Oeverboe K;

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fragment of a nucleic acid encoding a putative microbial virulence factor for the identification of a disease caused by mutations or for a genetic predisposition. The invention also relates to a method for identification of a disease caused by mutations or for a genetic predisposition. The invention also relates to a method for identification of a disease which comprises detecting the presence of a mutation within an uncleic acid sequence of the fragment of virulence factor in a tissue. The holod sample of a subject, where the issue sample is a foctal graft for neurotransplantation and where the sequence is inserted in the 3' company and a subject, where the sequence is inserted in the 3' company and a grasse caused by mutation or for their genetic predisposition of a disease caused by mutation or for their genetic predisposition of a disease caused by mutation or for their genetic predisposition of a disease, schizophrenia, myopathy, other forms of dementias. Parkinson's disease, schizophrenia, myopathy, other forms of dementia, cannath, hereditary multi-infarct dementia, the pathological constitutes a predisposition or a genetic variation, the pathological constitutes a predisposition or a genetic variation, the pathological constitutes a predisposition or a genetic variation, the pathological constitutes a predisposition or a genetic variation, the pathological cander the manifestation comprises any forms of ementia, schizophrenia or regulation comprises any forms of endocrates the manifestation discontant or regulation or regulation comprises any form the identifying or screening of compounds that have an effect on the cativity, expression or regulation or sequence is salmonal at the invention (ES) protein). The present sequence is salmonal at the invention described by invention of the pagence of the p
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                                                                                                                                                                                                                                                                                                 Use of DNA sequence having fragment of nucleic acid encoding putative microbial virulence factor useful for identification of disease e.g. Alzheimer's disease, caused by mutations or for genetic predisposition
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100.0%; Pred. No. 4.1e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 21; 52pp; English.
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                                              15-FEB-2001; 2001WO-IB00189
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nes 13; Conservative
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                                                                                                                                                  (FRIT/) FRITZSCHE M
                                                                                                                                                                                                                                                      WPI; 2002-241910/29
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WO200290374-A1.
                                                                the invention.
      Homo sapiens.
            14-NOV-2002.
    FragX 3; ss
                                sample
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ö Query Match 1.0%; Score 13; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 4.1e+02; Matches 13; Conservative 0; Mismatches 0; Indels Sequence 18 BP; 5 A; 2 C; 6 G; 5 T; 0 other; 799 TGCCATAAAGTCA 811 ò

14 TGCCATAAAGTCA 2 g

Haematopoietic cell proliferation disorder related oligonucleotide #1202. Human, haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; ABZ11062 standard; DNA; 18 BP (first entry) 16-JAN-2003 ABZ11062; ABZ11062/ 1D ABZ1: XX AZ ABZ1: XX DT 16-JJ XX Haem XX KW Human XW Gene RESULT

cytosine methylation state; probe; primer; ss.

Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J; Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E; Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T; Pelet C, Schwope I, Ziebarth H; Claim 15; Page 78; 117pp; English. 26-MAR-2002; 2002WO-BP03401. 26-MAR-2001; 2001US-278333P. (EPIG-) EPIGENOMICS AG. WPI; 2003-018942/01. WO200277272-A2 dimuclectides Homo sapiens. Synthetic. 03-OCT-2002. The invention relates to a method for identifying the presence or absence of a mutation or polymorphism in a plurality of genes. The method is used for identifying the presence or absence of a mutation or polymorphism in subject to the presence or absence of several genetic markers in a subject for diagnosing genetic diseases, e.g. cystic fibrosis, Tay-sachs, camilial hypercholestrolaemia (FH), thalasseamia, sickle cell disease, phenylketomuria, galactosaemia, fragile X syndrome, haemophilia A, myotonic dystrophy, medium-chain acyl CoA dehydrogenase, maturity onset diabetes, cystinuria, methylmolonic acidaemia, urea cycle disorders, thereditary fructose intolerance, hereditary haemachromatosis, neonatal thrombocytopaenia, Gauchers disease, tyrosinaemia, Wilson's disease, alcaptomuria, hypolactasia, Baker's disease, arginihaemia adenomatcous coli (ARC), adult polycystic kidney disease, bochenne muscular dystrophy, alpha-1-antitrypsin deficiency, hereditary non-polyposis colecceal cancer, Huntington's disease, neurofibromatosis, harian's colecceal cancer, Huntington's disease, neurofibromatosis, syndrome, osteogeneeis imperfecta, retinoblastoma, Freidrich's ataxia, haemoglobinopathies, MCAD, Canavan's disease, Leber's hereditary optic neuropathy, retinitis pigmentosas, Bloom syndrome, Panconi's anaemia, or Neimann Pick's disease. The present sequence is human Fragile X gene exon 3 (FragX 3) specific PCR primer used to illustrate the method of Gauchers disease; Canavan's disease; galactosaemia; thrombocytopaemia; thalassaemia; sickle cell disease; phenylketomuria; Marfan's syndrome; haemoglobinopathy; Bloom syndrome; Neimann Pick's disease; PCR; primer; Identifying the presence or absence of a mutation or polymorphism in a subject, useful for diagnosing genetic diseases, comprises generating extension products and analyzing the melting behavior of the mixed DNA Claim 56; Page 42; 49pp; English. (AMBR-) AMBRY GENETICS CORP. 06-MAY-2002; 2002WO-US14562 08-MAY-2001; 2001US-0851501 Dunlop CLM, Weisel JM, WPI; 2003-103498/09.

The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a bological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG which distinguishes between methylated and non-methylated CpG the control of 1.0%; Score 13; DB 1; Length 18; 100.0%; Pred. No. 4.1e+02; tive 0; Mismatches 0; Indels Sequence 18 BP; 4 A; 0 C; 3 G; 11 T; 0 other; 13; Conservative Local Similarity Query Match Matches ö Gaps

ö Human interleukin-1 beta oligonucleotide SEQ ID NO:305. ABL46338 standard; DNA; 30 BP. 1205 TTAAACAAACAAA 1217 26-APR-2002 (first entry) 15 TTAAACAAACAAA 3 ABL46338; RESULT 487 ABL46338
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AC ABL4
AC ABL4
DT 26-A
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The present invention describes a method for identifying oligonucleotides with desired hybridisation properties to nucleic acid targets containing secondary structure. The method comprises amplifying a target nucleic acid having at least one accessible and one inaccessible site. Primers that form an extension product are identified as the oligonucleotides which can interact with the folded target nucleic acid. Oligonucleotides from the present invention can be used in novel detection methods for clinical diagnostic purposes, including the detection and identification of pathogonic organisms (e.g. HIV). The method allows the ability to rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                      Identifying oligonuclectides hybridizing to nucleic acids containing secondary structure, useful in clinical diagnosis, comprises identifying primers that interact with the target to form an extension product under amplification conditions.
Nucleic acid accessible hybridisation site; detection; hybridisation; characterisation; identification; nucleic acid structure; diagnosis; PCR primer; probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.0%; Score 13; DB 1; Length 30; 76.2%; Pred. No. 5.6e+02; Live 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                               (THIR-) THIRD WAVE TECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 48; Fig 81A; 409pp; English
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                                                                           Homo sapiens
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PCR primers AA228411-Z28412 are used to amplify the microsatellite markers associated with the allele situated on chromosome 2, containing the D2S340 locus. The D2S340 microsatellite markers are contained in the region of chromosome 2 containing the IL2 (interleukin 2) cluster of
                                                                                                                                                                                            This invention describes a novel isolated nucleic acid (A) for the Neiseria gonorrhoeae GC-3 sequence. The isolated nucleic acid (A) and fragments of (A) are used for the species-specific detection of services of sequence in standard amplification or hybridization assays. Fragments of (A) are species-specific with no detectable cross-reaction with any other species, so they provide a rapid, reliable and selective fown to 10 genomic copies) diagnosis. AAZ24068-Z24090 represent PCR primers used in the identification of the N. gonorrhoeae GC3 fragment described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosing asthma, or an asthmatic predisposition, from the presence of specific alleles at a locus on chromosome 2\,
                                                                                                                     Isolated nucleic acid for the GC-3 fragment from Neisseria gonorrhoeae, useful for species-specific detection
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      asthma; predisposition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer UD2S340 used to amplify the D2S340 microsatellite marker.
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                                                                                                                                                                                                                                                                                                                                                                              Length 16;
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chromosome 2; genetic polymorphism; D2S340; detect; ss.
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                                                                                                                                                                                                                                                                                                                                                                              Score 12.8; DB 1;
Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                   Sequence 16 BP; 5 A; 3 C; 4 G; 4 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                  Claim 3; Page 28; 37pp; German
                              (BECT.) BECTON DICKINSON & CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         756 TGATATTTGAAGCATC 771
                                                                                                                                                                                                                                                                                                                                                                              1.0%;
98US-0067773.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Best Local Similarity 87.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-601341/51.
                                                                                          (PI; 1999-602549/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ28412 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cookson WOCM,
 27-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                           rou O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     489
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AAZ28412/
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Gaps ö

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genes. The invention relates to a method for diagnosing asthma or a predisposition to asthma. The products of PCR primers AA228409-228418 are used to detect amy alleles that may be connected with asthma. The D2S308*3 allele (PCR primers AA228409-228410 are used to amplify the associated microsatellite markers) is used in the claimed methods to identify children at risk of developing asthma by examination immediately after birth, potentially allowing the disease to be prevented. The methods may also allow a prognosis of the severity of a condition and responses to particular treatments.
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Sequence 16 BP; 1 A; 5 C; 3 G; 7 T; 0 other;

ô 1.0%; Score 12.8; DB 1; Length 16; 87.5%; Pred. No. 4.1e+02; tive 0; Mismatches 2; Indels 685 GCAAAATTGGGCCAAG 700 14; Conservative Best Local Similarity Query Match Matches Š

16 GCAAAACTGGGCAAAG 1 된

AAI67028 standard; DNA; 16 11-FEB-2002 AA167028; RESULT 490

BP

Human PLSCR1 intron 5/exon 6 junction sequence. (first entry)

Phospholipid scramblase; PLSCR; membrane protein; virucide; vaccine; cytostatic; leukemia; cancer; PLSCR1; human; ss.

Homo sapiens

WO200174295-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US10388.

31-MAR-2000; 2000US-193939P.

(SCRI) SCRIPPS RES INST. (CLEV-) CLEVELAND CLINIC POUND.

Sims PJ, Silverman RH, Wiedmer T;

WPI; 2001-626334/72.

Novel membrane proteins, phospholipid scramblase polypeptides, useful for treating and preventing cancer and viral infections, are induced by interferons

Example 8; Page 61; 94pp; English.

The invention provides phospholipid scramblase (PLSCR) polypeptides and polynucleotides encoding them. PLSCR are membrane proteins that mediate accelerated trans-bilayer movement of plasma membrane phospholipids in response to elevated cytoplasmic calcium. The PLSCR polypeptides are useful for inhibiting or preventing viral infection (e.g. infection of a membrane-bound virus or virus such as rhabdovirus, filovirus, retrovirus, flavirus, coronavirus, orthomyxovirus, baramyxovirus, retrovirus, herpesvirus, poxvirus, togavirus, iridovirus, paramyxovirus, aremavirus, HIV, Ebola virus, Marburg virus and Rabies virus). The polynuclectides are useful for treating aviral such as useful for treating a subject having or at risk of having a disorder modulating the PLSCR activity, are useful for treating infection or encourage in a plasma, chronic myelogenous lenkemia, myeloma, melanoma, renal cell lenkemia, chronic myelogenous lenkemia, myeloma, melanoma, renal cell carcinoma, Kaposi's sarcoma, follicular lymphoma, thrombocythemia or erythroleukemia, PLSCR is also useful for treating and preventing cancer. Sequences AMI670194-34 represent human PLSCRI

exon/introm junction sequences.

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Sequence 16 BP; 4 A; 1 C; 2 G; 9 T; 0 other;

Gaps ö Length 16; 1.0%; Score 12.8; DB 1; Length 1 17.5%; Pred. No. 4.1e+02; ve 0; Mismatches 2; Indels 1 Similarity 87.5%; 14; Conservative Local Similarity Query Match Matches

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à ద RESULT 491 AAD15192

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Gaps

AAD15192 standard; DNA; 16 BP.

AAD15192;

(first entry) 01-NOV-2001 5' RT-PCR primer for rabbit REC1_22 clone.

Party lesion development, atherosclerosis, Alzheimer's disease, nervous system disorder; Parkinson's disease; immune system disorder; tachemia; lymphopaenia; leukocyte adhesion deficiency syndrome; haemoglobinuria; ansemia; hyperproliferative disorder; Gaucher's disease; coagulation disorder; blood platelet disorder; autoimmune disorder; dermatitis; herpes simplex; Addison's disease; rheumatoid arthritis; drave's disease; gene therapy; antiatteriosclerotic; immunostimulant; cardiovascular; antiviral; RT-PCR primer; rabbit; ss.

Oryctolagus cuniculus.

WO200154651-A2.

02-AUG-2001

25-JAN-2001; 2001WO-US02439.

(DIGI-) DIGITAL GENE TECHNOLOGIES INC.

25-JAN-2000; 2000US-0177963.

Hasel KW; Glass JR, Sutcliffe JG, Leonardi A, Sartani A,

WPI; 2001-514526/56.

New polynucleotides regulated by fatty lesion development and their encoded polypeptides, useful for preventing, treating or ameliorating atherosclerosis, as well as for immune or hyperproliferative disorders

Example 2; Page 124; 188pp; English.

The present invention relates to an isolated nucleic acid regulated by fatty lesion development, which comprises any of 55 polymucleotide caquences from Orycolagus cuniculus. The polymucleotide, polypeptide or antibody is useful for preventing, treating, modulating or ameliorating a medical condition, particularly atherosclerosis. The invention is used as marker or detector of nervous system disorder or disease (e.g. Parkinson's disease, Alzheimer's disease, ischaemia, dementia). The invention may also be useful for treating deficiencies or disorders of the immune system (e.g. lymphopsenia, leukocyte adhesion deficiency syndrome or haemoglobinuria, anaemia), hyperproliferative disorders (e.g. daucher's disease), infectious disease (e.g. herpes simplex), coagulation disorders, blood platelet disorders and autoimmune disorders (Addison's disease, rheumatoid arthritis, dermatitis, Grave's disease). The polymuchotide sequence is also used in gene therapy. The present sequence is a 5' RT-PCR primer for rabbit RECI_22 clone.

Sequence 16 BP; 0 A; 6 C; 5 G; 5 T; 0 other;

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                             Gaps
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                                                                                                                                                                                                                                       Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bor-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
                                                                                                                                                                                                                 Rat ICAM hammerhead ribozyme target sequence (nt. position 2906)
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   1.0%; Score 12.8; DB 1; Length 16; 77.5%; Pred. No. 4.1e+02; ve 0; Mismatches 2; Indels
                                                  897 GIGCCTTGGTTTCTCC 912
                                                                                                                                   AATS3752 standard; RNA; 17 BP.
                                                               1 GGGCCTTGGCTTCTCC 16
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94US-021109-94US-021109-94US-0222795.
94US-0222795.
94US-022795.
94US-022795.
94US-0279193.
94US-0291932.
94US-0291433.
94US-0291433.
94US-0291433.
94US-0291433.
94US-0291433.
94US-0291433.
94US-0311749.
94US-0311749.
94US-0311749.
94US-0311749.
94US-0311749.
                87.5%;
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                                                                                                                                                                               (updated)
{first entry)
Query Match
Best Local Similarity 87.59
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     Rattus rattus
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03-APR-1997
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07-OCT-1994;
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23-DEC-1994;
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54-NOV-1994
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The present sequence represents the preferred target sequence for an enzymatic nucleic acid, especially a harmerhead ribozyme, which cleaves the human c-myb sequence at the base position indicated in the descriptor line. The c-myb sequence was screened for optimal ribozyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human c-myb hammerhead ribozyme target sequence (nt. position 2715).
                                                                                                                                     The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mERNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential harmershead and hairpin structures and that contain potential harmershead and hairpin. Ribozymes cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the ICAM-1 target sequences and thereby inhibit ICAM-1 expression, making them useful for reducing transplant rejection and alleviating symptoms in patients with themmatoid arthritis, asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New enzymatic nucleic acid molecules - which cleave RNA produced by e.g. c-myb, for treating restenosis or cancer
                                                   Ribozymes having modified bases and methods for producing them for use in inhibiting disease related genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bnzymatic nucleic acid; hammerhead; ribozyme; cleavage; human;
smooth muscle cell; hyperproliferation; restenosis; cancer;
c-myb; coronary angioplasty; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 1.0%; Score 12.8; DB 1; Length 17; Local Similarity 31.2%; Pred. No. 4.3e+02; Loss 5; Conservative 9; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Draper K, Jarvis T, McSwiggen J, Stinchcomb DT;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 5 A; 0 C; 3 G; 9 U; 0 other;
                                                                                                        Claim 2; Page 204; 407pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 77; 128pp; English.
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UUGAUGUAUUUAUUAA 17
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94US-0245466,
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               WPI; 1995-351090/45
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schultz143-3.rng

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Gaps

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which did not form secondary folding algorithm, and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme cleavage sites were identified. Ribozymes were synthesised and their activities optimised by either varying the length of the binding arms or by modification to prevent degradation by nucleases. The ribozymes cleave the c-myb sequence and can be used to prevent smooth muscle cell hyperproliferation in restenosis, especially after coronary angioplasty, and in cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNM encoding 1 or more receptors of vascular endothelial growth factor (VBGF). A patient (preferably human) having a condition associated with the level of the fim-like tyrosine kinase ! (fit-1), kinase innert domain containing receptor (KDR) and/or foetal liver kinase il (fit-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the mucleic acid molecule or the expression vector to the patient. AMK67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vascular endothelial growth factor receptor; VBGF receptor; flt-1; flt.1; KDR; hammerhead ribozyme; haltpin ribozyme; oleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fumour tyrosine kinase 1; kinase insert domain containing receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient
                                                                                                                                                                                                                                               2; Indels 0;
                                                                                                                                                                                                            Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human KDR VEGF receptor hammerhead ribozyme substrate #487.
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                                                                                                                                                                                                            Score 12.8; DB 1;
Pred. No. 4.3e+02;
                                                                                                                                                                         Sequence 17 BP; 7 A; 0 C; 0 G; 10 U; 0 other;
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(RIBO-) RIBOZYME PHARM INC.
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Best Local Similarity 87.5'
Matches 14, Conservative
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Seguence 17 BP; 7 A; 0 C; 4 G; 6 U; 0 other;

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56.2%; Pred. No. 4.3e+02;
tive 5; Mismatches 2;
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1.0%; Score 12.8; DB 1;
56.2%; Pred. No. 4.3e+02;
tive 5; Mismatches 2
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AAX71100
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fms-like tyrosine kinase 1; kinase insert domain containing receptor,
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(RIBO-) RIBOZYME PHARM INC.
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            foetal liver kinase 1; ss.
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                                                                                      Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogeneals; psoriasis; rheumatoid architius; coular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor; foetal liver kinase 1; ss.
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                                                                          Human KDR VEGF receptor hammerhead ribozyme substrate #112.
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AAX71100 standard; RNA; 17
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nes 8; Conservative
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the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VBGF). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAK67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention.
                                                                                                                                                                                                                                                                the present invention describes nucleic acid molecules which modulate
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                                                                                                  Nucleic acid molecule modulating VBGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient
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87.5%; Pred. No. 4.3e+02;
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  Escobedo J, McSwiggen J, Pavco P,
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87.5%; Pred. No. 4.3e+02;
tive 0; Mismatches 2; Indels
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(RIBO-) RIBOZYME PHARM INC.
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95US-0005974
                                                                            (CHIR ) CHIRON CORP.
(RIBO-) RIBOZYME PHARM INC.
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The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VRGF). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (fit-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (fik-1) (e.g. tumour
                                                                                                                                                           The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (WGGF). A patient (preferably human) having a condition associated with the level of the fims-like tyrosine kinase 1 (fit-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (fik-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention.
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mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17 BP; 3 A; 3 C; 0 G; 11 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 68; 218pp; English.
                                                                                                       Claim 4; Page 80; 218pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1085 ATTTGGAAAATAGAA 1100
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95US-0005974.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX69416 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escobedo J, McSwiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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26-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX69416;
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Solanidine; glucosyltransferase; potato; citrate synthase; target; hammerhead ribozyme; hairpin ribozyme; alkaloid biosynthesis; flower formation; cleavage; solanaceous plant; ss.

Solanum tuberosum.

WO9832843-A2

Potato citrate synthase target sequence position 1334.

(first entry)

01-MAR-1999

AAV96640;

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AAV96640 standard; RNA; 17

AV96640

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anglogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention.
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New hairpin and harmer:head ribozyme(s) - which inhibit abnormal smooth muscle cell proliferation in vascular tissue, partic. for preventing or treating restenosis
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribozyme; hairpin; hammerhead; recognition site; cdc2 kinase; restenosis; growth factor; oncogene; vascular tissue; smooth muscle cell proliferation; ss.
                                                                                                                                                                                                                                                     Length 17;
                                                                                                                                                                                                                                                  1.0%; Score 12.8; DB 1; Length 17 87.5%; Pred. No. 4.3e+02; vative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic cdc2 kinase ribozyme recognition site #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 7 A; 2 C; 1 G; 7 T; 0 other;
                                                                                                                                                                                 Sequence 17 BP; 3 A; 5 C; 1 G; 8 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with SMC growth following vascular injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 15; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     1586 ATGGAATATAAAAGT 1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US1483B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 Arggaagaraaggr 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT60201 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                       Local Similarity 87.5
1es 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goldenberg T, Tritz R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-202230/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMMU-) IMMUSOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT60201;
                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 501
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ID AAT60201/

AX AAT60201/

AX AAT61

AX AAT61

AX AAT61

AX AAT61

AX AAT60201/

AX AAT6
           88888
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New enzymatic nucleic acid(s) - useful for, e.g. reducing alkaloid

biosynthesis or regulating flowering

97US-0979416. 97US-0036545. 97US-0036599.

28-JAN-1997;

24-NOV-1997;

(RIBO-) RIBOZYMB PHARM INC.

McSwiggen JA, Zwick MG; WPI; 1998-427939/36.

98WO-US00738

14-JAN-1998;

30-JUL-1998

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The present invention describes enzymatic nucleic acid molecules with CC RNA-cleaving activity (e.g. ribozymes) which are capable of modulating carpression of plant genes: (i) involved in biosynthesis of alkaloids; or (ii) involved in flower formation. AAV95982 to AAV96334, and AAV96335 to AAV96334 represent potato solanidine glucosyltransferase campa AAV96355 to AAV96734 represent potato solanidine glucosyltransferase target sequences. AAV96773 represent potato solanidine glucosyltransferase target sequences. AAV96773 to AAV97170, and AAV97171 to AAV97195 corpresent potato citrate synthase hammerhead and hairpin ribozymes. respectively. AAV96773 to AAV96772, and AAV97195 to AAV97195 to AAV97195 corpresent potato citrate synthase hammerhead and hairpin ribozymes. CC represent potato citrate synthase hammerhead and hairpin ribozymes. CC represent potato citrate synthase hammerhead and hairpin ribozymes of toxic alkaloids in solanaceous plants, particularly potato but also tomato, pepper, caubergine and ditura or to inhibit flowering in potato, lettuce, spinach, caubergine and ditura or to inhibit flowering in potato, lettuce, spinach, cabbage, bruses practic and turf grass. Also the ribozymes can be used for RNA manipulation in the same way that restriction endonucleases are for DNA, as well as to examine genetic drift and mutations in plants and to detect specific RNA. The ribozymes can be targeted to specific genes or to consensus sequences within a family of related genes, and being corporations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 1.0%; Score 12.8; DB 1; Length 17; Local Similarity 43.8%; Pred. No. 4.3e+02; Local Sincles 7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 5 A; 1 C; 4 G; 7 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 53; Page 56; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1283 TTATTGTTTATCTGAA 1298
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Matches
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AAV95779 standard; RNA; 17 BP

AAV95779 ID AAV9

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Gape

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.Match 1.0%; Score 12.8; DB 1; Length 17; Local Similarity 87.5%; Pred. No. 4.3e+02; tes 14; Conservative 0; Mismatches 2; Indels

Query Match

Matches

1172 ITTATTAGATAAATTT 1187

16 TTTAATAGAGAATTT 1

RESULT 502

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New enzymatic nucleic acid(s) - useful for, e.g. reducing alkaloid biosynthesis or regulating flowering
                                            Solanidine, glucosyltransferase, potato, citrate synthase, target, hammerhead ribozyme, hairpin ribozyme, alkaloid biosynthesis; flower formation; cleavage; solanaceous plant; ss.
                             Solanidine glucosyltransferase target sequence position 579.
                                                                                                                                                                                                                                       Claim 13; Page 47; 79pp; English.
                                                                                                                                      97US-0979416.
                                                                                                                       98WO-US00738
                                                                                                                                             97US-0036545.
                                                                                                                                                                    (RIBO-) RIBOZYME PHARM INC.
               01-MAR-1999 (first entry)
                                                                                                                                                                                   Zwick MG;
                                                                                                                                                                                                  WPI; 1998-427939/36.
                                                                          Solanum tuberosum.
                                                                                                                                                                                   McSwiggen JA,
                                                                                                                       14-JAN-1998;
                                                                                         WO9832843-A2
                                                                                                                                      24-NOV-1997;
                                                                                                                                             28-JAN-1997;
                                                                                                        30-JUL-1998
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The present invention describes enzymatic nucleic acid molecules with RNA-cleaving activity (e.g. ribozymes) which are capable of modulating the expression of plant genes: (1) involved in bioxymthemis of and Anaybodis or (ii) involved in flower formation. AAV95982 to AAV96334, and AAV963154 represent potato solanidine glucosyltransferase hammerhead and hairpin ribozymes, respectively. AAV96325 to AAV95981, and AAV96325 to AAV96734 represent potato solanidine glucosyltransferase target sequences. AAV9673 to AAV97170, and AAV97171 to AAV97195

ceptesent potato citrate synthase harmerhead and hairpin ribozymes, respectively. AAV96735 to AAV96732, and AAV97196 to AAV97120 represent potato citrate synthase target sequences. Ribozymes of the present cotato citrate synthase target sequences. Ribozymes of the present citrate synthase target sequences. Ribozymes of the present citrate synthase target sequences. Ribozymes of the present citrate synthase target sequences. Ribozymes can didute or to inhibit flowering in potato, lettuce, spinach, cabbage, brussel sprouts, arugula, kale, collard, beet, turnip, sweet potato and turf grass. Also the ribozymes can be used for RNA manipulation in the same way that restriction endomucleases are for DNA, a well as to examine genetic drift and mutations in plants and to the consenus sequences within a family of related genes or to consenus sequences within a family of related genes, and being catalytic need to be present at only very low concentrations. Sequence 17 BP; 8 A; 1 C; 4 G; 4 U; 0 other;

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V Match 1.0%; Score 12.8; DB 1; Length 17; Local Similarity 62.5%; Pred. No. 4.3e+02; Ass 10; Conservative 4; Mismatches 2; Indels
                                                                                       1175 ATTAGATAAATTTCAA 1190
                                                                                                           2 AUGAGAUAAAGUUCAA 17
  Query Match
                                             Matches
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AAV24553 standard; DNA; 17 BP 16-SEP-1998 (first entry) AAV24553; RESULT 504 AAV24553

DNA polymerase; HBV; RNA intermediate; nucleotide analogue sensitivity; surface antigen interaction; sAg; antibody interaction; PCR primer; anti-viral therapy; ss. PCR primer for DNA polymerase fragment coding sequence.

Synthetic. Hepatitis b virus.

W09821317-A1.

22-MAY-1998.

97WO-AU00520. 15-AUG-1997;

(WHEA-) WESTERN HEALTH CARE NETWORK.

Locarnini SA; De Man RA, Aye TT, Bartholomeusz AI,

WPI; 1998-297924/26.

Variants of DNA virus replicating through RNA intermediate, especially hepatitis B - have mutations in genes for DNA polymerase, surface antigen or region of overlapping reading frames, and show reduced sensitivity to antiviral agents or antibodies

Example 3; Page 19; 53pp; English.

This sequence is a PCR primer for DNA encoding a fragment of a Hepatitis b virus (HBV) DNA polymerase. The amplified fragment can be mutated to give the variant of a DNA virus of the invention, that replicates via an RNA intermediate. Detection of mutations in the encoded protein sequence can be used in a method for determining if a HBV isolate has reduced sensitivity to a nucleotide analogue or if its surface antigen (SAG) has reduced interaction with antibodies. Mutations in the DNA polymerase gene indicate (partial) resistance to nucleotide analogues while those in the SAG gene indicate reduced interaction with specific antibodies. Detecting sequences containing these mutations is used to monitor anti-viral treatments (chemotherapy and/or vaccination) and to screen for agents that can overcome the effects of such mutations (potentially useful in long-term treatments with nucleotide analogues).

Sequence 17 BP; 5 A; 4 C; 1 G; 7 T; 0 other;

0; Gaps 1.0%; Score 12.8; DB 1; Length 17; 87.5%; Pred. No. 4.3e+02; ive 0; Mismatches 2; Indels Local Similarity 87.5 nes 14; Conservative Query Match Matches

1556 CTCCAAATTTTTTTA 1571 CICCAAATICTITATA 17 g ઠ

AAV24555 Btandard; DNA; 17 BP 16-SEP-1998 (first entry) AAV24555; RESULT 505 ZXZZZZZZZXZXZ X

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Gaps

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PCR primer for DNA polymerase fragment coding sequence.

DNA polymerase; HBV; RNA intermediate; nucleotide analogue sensitivity; surface antigen interaction; sAg; antibody interaction; PCR primer; anti-viral therapy; ss.

Synthetic. Hepatitis b virus.

WO9821317-A1

22-MAY-1998

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This sequence is a PCR primer for DNA encoding a fragment of a mutated to virus (HBV) DNA polymerase. The amplified fragment can be mutated to give the variant of a DNA virus of the invention, that replicates via an RNA intermediate. Detection of mutations in the encoded protein sequence can be used in a method for determining if a HBV esplate has reduced sensitivity to a nucleotide analogue or if its surface antigen (sAg) has reduced interaction with antibodies. Mutations in the DNA polymerase gene indicate (partial) resistance to nucleotide analogues while those in the sAg gene indicate reduced interaction with specific antibodies. Detecting sequences containing these mutations is used to monitor anti-viral treatments (chemotherapy and/or vaccination) and to screen for agents that can overcome the effects of such mutations (potentially useful in long-term treatments with nucleotide analogues).
                                                                                                                                                                                                                                                                                              Variants of DNA virus replicating through RNA intermediate, especially hepatitis B - have mutations in genes for DNA polymerase, surface antigen or region of overlapping reading frames, and show reduced sensitivity to antiviral agents or antibodies
                                                                                                                                                                                                                Bartholomeusz AI, De Man RA,
                                                                                                                                                                     (WHEA-) WESTERN HEALTH CARE NETWORK.
                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 19; 53pp; English.
                                                                                                                              96AU-0003519.
                                                                                    97WO-AU00520
                                                                                                                                                                                                                                                         WPI; 1998-297924/26.
                                                                                                                              08-NOV-1996;
                                                                                    15-AUG-1997;
                                                                                                                                                                                                                Aye IT,
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1.0%; Score 12.8; DB 1; Length 17; 87.5%; Pred. No. 4.3e+02; vative 0; Mismatches 2; Indels Sequence 17 BP; 5 A; 4 C; 1 G; 7 T; 0 other; 1556 CICCAAATITITITA 1571 crecaaarrerrara 17 Local Similarity 87.5 nes 14; Conservative Query Match ठ 셤

RESULT 506

AAA18614 Standard; RNA; 17 AAA18614;

19-JUN-2000 (first entry)

Human TIE-2 substrate sequence SBQ ID NO:1840.

Human; aryl hydrocarbon nuclear transport; ARNT; TIB-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidabetic; ophthalmologic; antiinflammatory; antiarthritic; antissoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verucac vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Rippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss. AAA18614/AAA11D AAA11 XX AC AAA11 XX XX 19-J XX XX HUMB XX HUMB XX HUMB XX HUMB XX HUMB XX HUMB XX HOPET XX HOP

Homo sapiens

WO9950403-A2

07-0CT-1999.

99WO-US06507. 24-MAR-1999;

27-MAR-1998; 98US-0079678.

(RIBO-) RIBOZYME PHARM INC.

McSwiggen JA; Coeshott C, Jarvis T, Roberts E, Pavco PA,

WPI; 1999-591315/50.

expression and/or Novel ribozymes for modulating the synthesis, expresstability of an mRNA encoding an angiogenic factors

Claim 56; Page 106; 305pp; English.

Locarnini SA;

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl Nydrocarbon nuclear transporter (ARNY) gene, an integrin submuit beta 3 gene, an integrin submuit beta 3 gene, an integrin submuit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17167 and AAA1762 to AAA17622 represent ribozyme sequences for ARNY, corresponding target sequences; AAA19185 to AAA19185 and AAA19087 to AAA19184 represent ribozyme sequences for Tie-2, and AAA19185 to AAA19087 to AAA191221 represent their corresponding target sequences; AAA191221 to AAA21601 and AAA21601 and AAA21601 and AAA21601 and AAA21601 corresponding target sequences; AAA21609 to AAA21601 and AAA21601 corresponding target sequences; AAA21609 to AAA21605 and AAA21609 to integrin subunit alpha-6, or integrin subunit beta-3.

Sequence 17 BP; 6 A; 3 C; 2 G; 6 U; 0 other;

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Gaps

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Gaps ö Query Match 1.0%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 4.3e+02; Matches 14; Conservative 0; Mismatches 2; Indels 14; Conservative

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AAA18615 standard; RNA; 17 BP

AAA18615/

19-JUN-2000 (first entry) AAA18615;

Human TIE-2 substrate sequence SEQ ID NO:1841.

Human; aryl hydrocarbon nuclear transport; ARNT; TIB-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; antidialencic factor; cytostatic; antidiabetic; ophthalmologic; antilnflammatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; vertuce aulgaris; anglofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Rippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens

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The present invention describes enzymatic mucleic acid molecules with the RNA cleaving activity, which specifically cleave RNA encoded by an aryl RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon muclear transporter (ARNT) gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17167 and AAA17168 to AAA17650 and AAA1762 represent ribozyme sequences for AAA1918 to AAA2180 to AA
                                                                                                                                                                                                                                                                                                                                                                                      Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an anglogenic factors
                                                                                                                                                                                                                                                                             Coeshott C, McSwiggen JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  integrin subunit alpha-6, or integrin subunit beta-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 56; Page 106; 305pp; English.
                                                                                                                                                                                                                                                                             Jarvis T,
                                                                                                           99WO-US06507.
                                                                                                                                                                 98US-007967B
                                                                                                                                                                                                                       (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                             Roberts B,
                                                                                                                                                                                                                                                                                                                                   WPI; 1999-591315/50.
                                                                                                           24-MAR-1999;
                                                                                                                                                                 27-MAR-1998;
  WO9950403-A2
                                                     07-0CT-1999.
                                                                                                                                                                                                                                                                                   Pavco PA,
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Sequence 17 BP; 6 A; 3 C; 2 G; 6 U; 0 other;

Gaps ö Query Match
1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels ò

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RESULT 508

AAA21157 standard; RNA; 17 BP.

AAA21157;

Integrin alpha 6 subunit substrate seguence SEQ ID NO:4383. 19-JUN-2000 (first entry)

Human; aryl hydrocarbon nuclear transport; ARMT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic, antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;

. დ tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA; 99WO-US06507. 98US-0079678 (RIBO-) RIBOZYME PHARM INC. WPI; 1999-591315/50. 27-MAR-1998; 24-MAR-1999; WO9950403-A2. Homo sapiens 07-0CT-1999.

The present invention describes enzymatic nucleic acid molecules with CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNY) gene, an integrin subunit beeta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene, AAA16775 to CC AAA1767 and AAA1762 to AAA1762 to AAA1762 to AAA1762 to AAA1762 and AAA1763 to AAA1762 and AAA1768 represent their corresponding target sequences; AAA1763 to AAA19185 to AAA1967 to AAA19184 represent ribozyme sequences for Tie-2, and AAA1818 to AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA1818 to AAA19087 to AAA19155 to AAA19152 represent their corresponding target sequences; AAA19154 to AAA19159 to AAA21591 to AAA21595 represent ribozyme sequences for integrin alpha 6 subunit, and AAA21836 to AAA21680 and AAA2189 to AAA2168 represent their corresponding target sequences; AAA2189 to AAA2168 represent their corresponding target sequences; AAA2189 to AAA2168 to AAA2168 to AAA23163 to AAA2333 Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors $\,$ Claim 55; Page 190; 305pp; English.

Sequence 17 BP; 6 A; 2 C; 1 G; 8 U; 0 other;

Gaps ç Query Match
1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 43.8%; Pred. No. 4.3e+02;
Matches 7; Conservative 7; Mismatches 2; Indels

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1002 ATAACATAAATTATTT 1017 2 AUGACCUAAAUUAUUU 17 RESULT 509 AAA21200 g 8

Integrin alpha 6 subunit substrate sequence SEQ ID NO:4426. 19-JUN-2000 (first entry) AAA21200;

AAA21200 standard; RNA; 17 BP

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; anglogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;

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Homo sapiens.
          WO9950403-A2
              24-MAR-1999;
                 27-MAR-1998;
            07-OCT-1999.
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hammerhead ribozyme, angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiniflammatory; antiatthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis, age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; peoriasis; verrues anigaris; angiofibrona; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; ss. Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss. Coeshott C, McSwiggen JA, stability of an mRNA encoding an angiogenic factors Jarvie T, 99WO-US06507. 98US-0079678. (RIBO-) RIBOZYME PHARM INC. Pavco PA, Roberts B, WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or

Claim 55; Page 193; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin subunit beta 3 gene, an integrin subunit beta 3 gene, and AAA1761 to AAA1762 represent ribozyme sequences for AAA1767 to AAA19154 represent ribozyme sequences for Fie-2, and AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA19087 to AAA19023 to AAA19022 represent their corresponding target sequences; AAA19023 to AAA19030 and AAA19023 to AAA19030 and AAA19023 to AAA19030 and AAA1068 to AAA21080 represent their corresponding target sequences; AAA21689 to AAA21680 represent their corresponding target sequences; AAA21689 to AAA21687 and AAA21631 and AAA21631 copresent ribozyme corresponding target sequences; C for integrin subunit beta 3, and AAA21342 represent ribozyme sequence for integrin subunit beta 3, and AAA21340 represent ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, cespecially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARND), inflammation, and arthritis, as well as corresponding orgiofilbrome of tuberous sclerosis, pot-wine stains, Sturge Weber Syndrome, Syndrome, Kippel-Trenaunay-Weber sparform, where syndrome, sparforms and diseases related to the levels of ARNT, Tie-2, increar and other syndromes enlared to the levels of ARNT, integrin chance, integrin control of the invention and disease related to the levels of ARNT, Tie-2, integrin controls and disease related to the levels of ARNT, Tie-2, integrin controls and disease related to the levels of ARNT, Tie-2, integring the syndrome of the levels of any order of the parts of ARNT, Tie-2, integring the syndrome of the levels of any order of the parts of ARNT, Tie-2, integring the syndrome of the levels of the integrin subunit alpha-6, or integrin subunit beta-3.

Sequence 17 BP; 3 A; 2 C; 4 G; 8 U; 0 other;

Gaps ö Length 17; Indela 1.0%; Score 12.8; DB 1; 13.8%; Pred. No. 4.3e+02; Ive 7; Mismatches 2; 7; Conservative Ouery Match Best Local Similarity Matches 7; Conserv

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UUUAUUCAGGCAUUG 17

AAA21469/C RESULT

722 TTAATTTCAGGAATTG 737 Š

19-JUN-2000 (first entry) AAA21469; BXXXB

AAA21469 standard; RNA; 17 BP

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNY) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17167 and AAA1762 represent ribozyme sequences for ARNY, corresponding target sequences, AAA17634 represent their corresponding target sequences, AAA17635 to AAA19154 represent ribozyme sequences for Tie-2, and AAA1938 to AAA1935 to AAA2195 represent their corresponding target sequences; AAA1935 to AAA21631 and AAA21601 and AAA2160 and AAA21689 to AAA2161 and AAA2160 to AAA2160 and CC Sequences for integrin alpha 6 subunit, and AAA2362 to AAA21360 and CC AAA21689 to AAA22167 and AAA2167 to AAA21635 represent ribozyme sequence for integrin subunit beta 3, and AAA22476 to AAA21361, AAA23343 to CC AAA21632 represent their corresponding target sequences the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNY, cc the invention are used for modulating the synthesis, expression and/or especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARWD), inflammation, and arthritis, as well as engleromes and others syndrome, Stippel-Trenauray-Weber syndrome, Osler Weber-Ronds and diseases related to the levels of ARNY, Tie-2, integrin subunit, all and the syndromes and diseases related to the levels of ARNY, Tie-2, integrin subunit, all and the syndromes and diseases related to the levels of ARNY, Tie-2, integrin subunit, all and the syndromes and diseases related to the levels of ARNY, Tie-2, integrin subunit, all and the syndromes and diseases related to the levels of ARNY, Tie-2, integrin subunit, all and the syndromes and diseases related to the levels of ARNY, Tie-2, integrin subunit, all and the availance of the stable to the arthress of ARNY, the arthr Human; aryl hydrocarbon nuclear transport; ARNT; TIB-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; harmerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsociatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; vertuca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss. Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors Pavco PA, Roberts E, Jarvis I, Coeshott C, McSwiggen JA; Integrin alpha 6 subunit substrate sequence SEQ ID NO:4695. Claim 55; Page 210; 305pp; English. 99WO-US06507. 98US-0079678 (RIBO-) RIBOZYME PHARM INC. WPI; 1999-591315/50. Homo gapiens. 24-MAR-1999; 27-MAR-1998; 409950403-A2

/ Match 1.0%; Score 12.8; DB 1; Length 17; Local Similarity 87.5%; Pred. No. 4.3e+02; nes 14; Conservative 0; Mismatches 2; Indels Sequence 17 BP; 9 A; 0 C; 0 G; 8 U; 0 other; Query Match

integrin subunit alpha-6, or integrin subunit beta-3.

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Gaps

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1133 TTATAGTAAATTTATT 1148 16 Transasasarriatr

Matches

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AAA21476/c RESULT 511

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Integrin alpha 6 subunit substrate sequence SEQ ID NO:4702. AAA21476 standard; RNA; 17 (first entry) 19-JUN-2000 AAA21476;

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; harmerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermarblogical; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verruca vulgaris; angiofibroma; tuberous solerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens.

W09950403-A2

07-0CT-1999.

99WO-US06507. 24-MAR-1999; 98US-0079678 27-MAR-1998;

(RIBO-) RIBOZYME PHARM INC.

Pavco PA, Roberts E, Jarvis F, Coeshott C, McSwiggen JA;

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors

Claim 55; Page 210; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl with cleaving activity, which specifically cleave RNA encoded by an aryl with activity, which specifically cleave RNA encoded by an aryl or an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17165 to AAA17651 to AAA17622 represent ribozyme sequences for AAA17635 to AAA19155 to AAA19155 to AAA19155 and AAA18385 and AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA19087 to AAA19087 and AAA19155 to AAA19222 represent their corresponding target sequences; AAA19223 to AAA21501 to AAA21505 represent ribozyme sequences; AAA21688 represent their corresponding target sequences; AAA21689 represent their corresponding target sequences; AAA21689 to AAA21675 and AAA21635 represent ribozyme sequences; AAA21689 represent their corresponding target sequences; AAA21689 represent their corresponding target sequences; AAA21689 to AAA21675 and AAA21675 to AAA21682 represent their corresponding target sequences; AAA21689 to AAA21675 and AAA22476 to AAA23262, AAA23431 to for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23431 to the invention are used for modulating the sequences. The ribozyme sequence of the invention are used for modulating the sequences the ribozyme of the mana encouraging angiogenic factor, especially ase related capencration (ARM), inflammation, and arthritis, as well as medular degeneration (ARM), inflammation, and arthritis, as well an encouraging the syndrome, Mippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndrome and diseases related to the levels of ARM1, Tie-2, and other syndromes and other syndromes are sequenced to the syndrome of integrin subunit alpha-6, or integrin subunit beta-3.

Sequence 17 BP; 4 A; 2 C; 3 G; 8 U; 0 other;

Gaps ö 1.0%; Score 12.8; DB 1; Length 17; 87.5%; Pred. No. 4.3e+02; tive 0; Mismatches 2; Indels Query Match
Best Local Similarity 87.5
Matches 14; Conservative

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16 AAACAATGAACACTTT

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RESULT 512 AAA227

AAA22708 standard; RNA; 17 BP

AAA22708;

19-JUN-2000 (first entry)

Integrin subunit beta 3 substrate sequence SEQ ID NO:5934.

Human; aryl hydrocarbon nuclear transport; ARNT; TIB-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antidnflammatory; antiarthritic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; poriasis; verruca vulgaris; angiofibroma; tuberous sclerosis; bot-wine stain; Sturge Weber syndrome; Rippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens

WO9950403-A2

07-0CT-1999.

99WO-US06507. 24-MAR-1999; 98US-0079678. 27-MAR-1998;

(RIBO-) RIBOZYME PHARM INC.

Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors

Claim 54; Page 237; 305pp; English.

The present invention the pecifically cleare RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin submit beta 3 and AAA1761 to AAA1762 represent ribozyme sequences for ARNT, and AAA17651 to AAA1762 and AAA1768 represent their submit their corresponding target sequences; AAA1768 to AAA1768 to AAA1768 to AAA1768 to AAA1768 to AAA1768 to AAA1969 to AAA1915 represent ribozyme sequences for Tie-2, and AAA1838 to AAA1908 to AAA1915 to AAA1915 and AAA1915 represent their corresponding target sequences; AAA1915 to AAA1915 and AAA2180 to The present invention describes enzymatic nucleic acid molecules with integrin subunit alpha-6, or integrin subunit beta-3

Sequence 17 BP; 3 A; 0 C; 1 G; 13 U; 0 other;

Query Match

1.0%; Score 12.8; DB 1;

539 AAACAATGAATAGTTT 554

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2; Indels

1.0%; Score 12.8; DB 1; 87.5%; Pred. No. 4.3e+02; iive 0; Mismatches 2;

546 GAATAGITTTTCATTG 561

14; Conservative

Query Match Best Local Similarity Matches 14; Conserv

17 GAATAGETHATCETEG

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Length 17;

or integrin subunit beta-3.

Sequence 17 BP; 8 A; 3 C; 1 G; 5 U; 0 other;

integrin subunit alpha-6,

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The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl Pydrocarbon nuclear transporter (ARNY) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16575 to AAA17167 and AAA1766 to AAA1768 to Fersent their corresponding target sequences; AAA1768 to AAA1885 and AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA18186 to AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA18186 to AAA1908 to AAA19155 to AAA19159 to AAA19155 to AAA191595 to AAA19159 to AAA18188 to AAA18189 to AAA2189 to A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; aryl hydrocarbon nuclear transport, ARNT; TIB-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic, antiinflammatory; antiarthritic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma;
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
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  18.8%; Pred. No. 4.3e+02; cive 11; Mismatches 2; Indels
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                                                                               1044 TTATTTATGTATTTAT 1059
                                                                                                                                                                                                                                                               AAA22776 standard; RNA; 17 BP
                                                                                                              UNACTURATED THE 16 TO THE TRANSPORTED TO
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Best Local Similarity 18.8
Matches 3; Conservative
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The present invention describes enzymatic nucleic acid molecules with RAG cleaving activity, which specifically cleave RNA encoded by an aryl Pydrocarbon nuclear transporter (ARNY) gene, an integrin submit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17167 and AAA17561 to AAA1762 represent ribozyme sequences for AAN1767 and AAA1768 to AAA1768 to AAA1768 to AAA1768 to AAA1768 to AAA1985 and AAA19087 to Corresponding target sequences for Tie-2, and AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA19087 to AAA19155 to AAA19152 represent their corresponding target sequences; AAA19155 to AAA19155 and AAA21850 to AAA21850 and AAA21850 to AAA21850 and AAA21850 to AAA21850 and AAA21850 to AAA21850 and AAA23283 to AAA21850 and AAA23363 to AAA23362 to AAA2333 t
                                                                                                                                                                                                                                                                                 Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; harmerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verrue andioxide angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
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                                                                                                                                                                                                                                   Integrin subunit beta 3 substrate sequence SEQ ID NO:6124.
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stability of an mRNA encoding an angiogenic factors
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                                                             AAA22898 standard, RNA, 17 BP
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                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-591315/50.
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                                                                                                                    AAA22898;
RESULT 514
AAA22898/c
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schultz143-3.rng

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RESULT 516
                 AAX80243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel isolated nucleic acid (A) for the Neisseria gonorrhoeae GC-3 sequence. The isolated nucleic acid (A) and fragments of (A) are used for the species-specific detection of Neisseria gonorrhoeae in standard amplification or hybridization assays. Fragments of (A) are species-specific with no detectable cross-reaction with any other species, so they provide a rapid, reliable and selective (down to 10 genomic copies) diagnosis, AAZ24068-Z24090 represent PCR primers used in the identification of the N. gonorrhoeae GC3 fragment described in the cethod of the invention.
macular degeneration (ARMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, angiofibroma of tuberous scleroals, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARMT, Tie-2, integrin subunit alpha-6, or integrin subunit beta-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid for the GC-3 fragment from Neisseria gonorrhoeae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GC3; species-specific detection; amplification; diagnosis; primer; ss.
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87.5%; Pred. No. 4.3e+02;
cive 0; Mismatches 2; Indels
                                                                                                                                                 ch 1.0%; Score 12.8; DB 1; Length 17; 1 Similarity 87.5%; Pred. No. 4.3e+02; 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    N. gonorrhoeae GC3 DNA fragment PCR primer 21.
                                                                                                                   Sequence 17 BP; 13 A; 0 C; 0 G; 4 U; 0 other;
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                                                                                                                                                                                                                        1045 TATTTATGTATTTATT 1060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                          AAZ24086;
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                                                                                                                                                        Query Match
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Matches
                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                            AAZ24086,
                                                                                                                                                                                                                                                                                                            RESULT
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The present invention describes fifteen new mutants of the breast cancer susceptibility gene BRCA1 gene, the mutations being located at mutleocides 421-2, 815, 926, 1050, 2034, 4483, 4643, 5053, 5210, 5396.460, 5150, 3904, 3888, 903, and 4164. AAX80255 to AAX80289 represent allele specific oligonucleotides for the mutant and wild type sequences of human BRCA1, and so are capable of identifying the normal or mutant end by hybridisation. Methods from the present invention may be used for detecting a predisposition to cancer, especially breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, BRCA1, wild type; mutant; detection; primer; probe; cancer;
breast cancer susceptibility gene; identification; variation;
hybridisation; breast cancer; ss.
                                                                         Human BRCA1 wild type allele specific oligonucleotide SEQ ID NO:17.
                                                                                                      Human, BRCA1; wild type; mutant; detection; primer; probe; cancer;
breast cancer susceptibility gene; identification; variation;
hybridisation; breast cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human BRCAl mutant allele specific oligonucleotide SEQ ID NO:18.
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                                                                                                                                                                                                                                                                                                                                                   Lescallett JL;
Thurber DB, White MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 6 A; 2 C; 3 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutants in BRCA gene associated with cancer
                                                                                                                                                                                                                                                                                                                                                   Lawrence T,
Sadzewicz LK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Page 64; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           524 AATTTGAATTTCAGTA 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX80244 standard; DNA; 17 BP
AAX80243 standard; DNA; 17 BP.
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                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                   Angelly TS,
Olson SJ,
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-385623/32.
                                                                                                                                                                                                                                                                                                                          (GENE-) GENE LOGIC.
                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                             11-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                   07-DEC-1998;
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                                                       18-AUG-1999
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                                                                                                                                                                   Synthetic.
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                              AAX80243;
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                                                                                                                                                                                                                                                                                                                                                                  Murphy P
Zeng B;
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756 TGATATTTGAAGCATC 771

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17 TGACATTTGACGCATC

L, Bellon L, Burgin A, Jarvis T; , Matulic-Adamic J, McSwiggen JA; Sweedler D, Thompson J, Workman CT;

(RIBO-) RIBOZYME PHARM INC.

Beigelman L,

Beaudry A,

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Human, c-raf, A-raf, B-raf, hammerhead ribozyme, hairpin ribozyme, target, substrate, catalyst, modulation, expression, Raf gene, delivery, screening, identification, synthesis, deprotection, purification, cancer, inflammation, poscriacis, non-hapatic ascites, inflection, genetic drift, restenosis, rheumatoid arthritis, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human C-raf target site nucleotide position 513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           524 AATTTGAATTTCAGTA 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        970S-0046059.
970S-0049002.
970S-0051718.
970S-0051321.
970S-0061324.
970S-0061324.
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                                                                                                                                                                                         WPI; 1999-385623/32.
                                                                                                              (GENE-) GENE LOGIC.
                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                               07-DEC-1998;
                                                                                     11-DEC-1997;
             WO9929903-A2
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02-OCT-1997;
05-NOV-1997;
                                     17-JUN-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-NOV-1998
                                                                                                                                                  Murphy PD,
Zeng B;
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                                                                                                                                       Allen AP,
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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AAV90992/C
AXX AAV90992/C
AXX AAV90
DXX 18-F9
XXX Humai
XXX 12-P0
PR 09-M
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capable of modulating a process in a biological system. The method capable of modulating a process in a biological system. The method comparises: (a) introducing into the system a random library of mucleic comparises: (a) introducing a substrate binding domain (SBD), comparising a random sequence, and a catalytic domain (CD); and (D) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDs in such systems. Nucleic acid molecules with endomuclease activity and catalytic activity, from the present invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases caused by specific RNA, e.g. cancer, inflammation, psortais, non-leagued and mutations in diseased cells and to determine careful systemic diseases caused by specific RNA, cleaving activity that modulate careful systemic diseases are set in an elle and to treat cancer, restences to periasis or rheumatoid arthritis, or generally any condition associated with the level of c-raf. Introduction of sugar/phosphate modifications in creases stability against nuclease and activity. Avy9922 to Avy93877 represent NACs that can be used in the method, specifically for modulating the expression of a Raf gene.
                                                                                                                                                                                                                                                                processes - especially ribozymes that cleave Raf RNA for treating cancer, restenosis, and also new ribozymes and modified nucleoside triphosphates used as antiviral agents and synthons
                                                                                                                                                                                                                                       Identifying new catalytic nucleic acid that modulates selected
                                                                                                                                                                                                                                                                                                                                                                             Claim 177; Page 147; 259pp; English.
                                                                                                         Kisich K,
                                                                                                      Karpeisky A, Kisich K
Parry T, Reynolds M,
                                                                                                                                                                                      WPI; 1999-009494/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes fifteen new mutants of the breast cancer susceptibility gene BRCA1 gene, the mutations being located at nucleotides 421-2, 815, 926, 1506, 2034, 4643, 4643, 5053, 5210, 5396,460, 5150, 3904, 3888, 993, and 4164. AAX80235 to AAX80289 represent allele specific oligonucleotides for the mutant and wild type sequences of human BRCA1, and so are capable of identifying the normal or mutant gene by hybridisation. Methods from the present invention may be used for detecting a predisposition to cancer, especially breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Thurber DB, White MB;
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                                                                                                                                                                                                                                                                                       Lawrence T,
Sadzewicz LK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Page 64; 118pp; English.
                                                                                                                             98WO-US25916.
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Olson SJ,
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                        Similarity 87.5%; Pred. No. 4.3e+02;
14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                              Juman C-raf target site nucleotide position 517.
Sequence 17 BP; 4 A; 4 C; 2 G; 7 U; 0 other;
                                                                                 446 AGCAAATCTACTTCAA 461
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                                                                                                        17 AGGAAATCTACTTGAA 2
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AAV90993 standard; RNA; 17
                                                                                                                                                                                                                                   (first entry)
                                     Local Similarion
ee 14; Conservative
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                          Query Match
                                                                                                                                                    RESULT 519
                                                     Matches
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11-APR-2000; 2000WO-US09721.

97US-0046059 97US-0049002

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The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TRS Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents thin bition (and consequently increases expression of) genes involved in the production of eryhmopoletin, granulocyte colony stimulating factor protein and interferon alpha.
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                                                                                                                                                                                                                    Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17 BP; 2 A; 2 C; 3 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McSwiggen J;
                                                                                                                                            McSwiggen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hammerhead ribozyme substrate #1617.
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                                                                                                                                                                                                                                                                                                              Claim 37; Page 73; 164pp; English.
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                                                                                                                                            Pavco P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAAACAAACAAACGA 1
                                                          99US-0129390.
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                                                                                                 (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-647423/62.
                                                                                                                                                                                  WPI; 2000-647423/62.
                                                                                                                                            Zwick M,
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                                                            12-APR-1999;
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                                                                                                                                              Blatt L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   capable of modulating a process in a biological system. The method capable of modulating a process in a biological system. The method comparises: (a) introducing into the system a random library of mucleic comparises: (a) introducing a substrate binding domain (SBD), comparising a random sequence, and a catalytic domain (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDs in such systems. Nucleic acid molecules with endomuclease activity and catalytic activity, from the present invention, are used to modulate gene expression in plant and mammalian calls and to cleave target mucleic acid, particularly for treating systemic diseases caused by specific RNA, e.g. cancer, inflammation, psortaisis, non-hepatic ascites and infection. They may also be used to pertains in diseased cells and to determine craft RNA. Specifically NACs with RNA-cleaving activity that modulate craft the level of c-raf. Introduction of sugar/phosphate modifications with the level of c-raf. Introduction of sugar/phosphate modifications in the method, specifically for modulating the expression of a Raf gene.
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                                                                                                                                                                                                                                                                                                                                         Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, restenosis, and also new ribozymes and modified nucleoside triphosphates used as antiviral agents and synthons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribozyme, erythropoletin; granulocyte colony stimulating factor;
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1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                               Beaudry A, Beigelman L, Bellon L, Burgin A, Jarvis T;
Karpeisky A, Kisich K, Matulic-Adamic J, McSwiggen JA;
Parry T, Reynolds M, Sweedler D, Thompson J, Workman CT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17 BP; 5 A; 2 C; 4 G; 6 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 177; Page 147; 259pp; English.
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                                             97US-0051718.
97US-0056808.
97US-0061321.
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                                                                                                          97US-0061324.
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                                                                                                                                                                           (RIBO-) RIBOZYMB PHARM INC.
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                                                                                                                                                                                                                                                                                                       WPI; 1999-009494/01
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                                             03-JUL-1997;
22-AUG-1997;
02-OCT-1997;
02-OCT-1997;
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                                                                                                                                   35-KOV-1997;
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RESULT 520

ઠે 셤 erythropoietin; granulocyte colony stimulating factor;

Hammerhead ribozyme substrate #2103.

interferon alpha; ss

Ribozyme;

(first entry)

16-FEB-2001

AAF04587;

AAF04587 standard; DNA; 17 BP.

RESULT 523

AAF04587

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molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, BR3/COUP-TP-1, the GATA transcription factor gene, IRP-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.
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                                                                                                                                                                                     1.0%; Score 12.8; DB 1; Length 1
87.5%; Pred. No. 4.3e+02;
tive 0; Mismatches 2; Indels
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87.5%; Pred. No. 4.3e+02;
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                                                                                                                                                  Sequence 17 BP; 6 A; 0 C; 2 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blatt L, Zwick M, Pavco P, McSwiggen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hammerhead ribozyme substrate #1653.
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                                                                                                                                                                                                                                                                                                                                                                                               AAF03358 standard; DNA; 17
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                                                                                                                                                                   Query Match
Best Local Similarity 87.5%
These 14; Conservative
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Best Local Similarity 87.5
Matches 14; Conservative
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The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, RAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, gramulocyte colony stimulating factor protein and interferon alpha.
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                                                                                                                                                                                                                                                                      McSwiggen J;
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les 14; Conservative
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                                                                                                                                                                                                                                                                      Zwick M,
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                                                                                                                  Homo sapiens.
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2; Indels

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985 CTTTAAGTTTTTTCAT 1000

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Matches
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                                                                                                                                                                     Buzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin -
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87.5%; Pred. No. 4.38+02;
.ive 0; Mismatches 2; Indels
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                                                                                                                 McSwiggen J;
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                                                                                                                                                                                                                              Claim 4; Page 111; 164pp; English.
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                                                                                                                   Pavco P,
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                                 11-APR-2000; 2000WO-US09721
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                                                                                      (RIBO-) RIBOZYMB PHARM INC.
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Best Local Similarity 87.5
Matches 14; Conservative
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                                                                                                                   Zwick M,
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      19-0CT-2000
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                                                                                                                   Blatt L,
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The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, BAR3/COUF-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents the production of exphroposietin, granulocyte colony stimulating factor protein and interferon alpha.
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useful for producing e.g. granulocyte colony stimulating factor
protein, interferon alpha and erythropoietin -
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Best Local Similarity
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L1-APR-2000; 2000WO-US09721.

19-0CT-2000

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The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McSwiggen J;
                                                                                                                                                                                                                                                                           Hammerhead ribozyme substrate #2730.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 118; 164pp; English
                                                                          AAF05511 standard; DNA; 17 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
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                                                                                                                                                                                                           16-FEB-2001 (first entry
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                                                                                                                                                                                                                                                                                                                                                                                      interferon alpha; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-647423/62.
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                                                                                                                                           AAF05511;
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AAF05511
AAF0511
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                                                                                                                                                                                                                                                                                      McSwiggen J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 42; Page 127; 164pp; English.
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                                                                                                                                                          99US-0129390.
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                                                                                                                                                          12-APR-1999;
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GapB

16 AGATAAAAAACAATTA 1

AAF06352 standard; DNA; 17

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Query Match
Best Local Similarity 37.5%;
Matches 6; Conservative
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                  The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TP-1, the GATA transcription factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha.
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                                                                                                                                                                                                                                            Sequence 17 BP; 4 A; 1 C; 1 G; 11 U; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                           1248 AGATAAACAACAATA 1263
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                                                                                                                                                                                                                                                                                                                                                                                                                                       17 AGATAAAAAACAATTA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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XX AAPO
XX AAPO
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XX AAPO
XX Bibo
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Gaps

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hairpin; hammerhead; gene therapy; vasotropic;

Ribozyme; hair restenosis; ss

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Gaps

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1248 AGATAAACAACAAATA 1263

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Mammalia

Cdc 2 kinase hammerhead ribozyme recognitoin site #2.

(first entry)

04-DEC-2000

AAA86571;

AAA86571 standard; DNA; 17 BP

Length 17; Indels

Score 12.8; DB 1; Pred. No. 4.3e+02; 8; Mismatches 2;

1527 TTTTTAACTITAAGAT 1542

1 UUUAUAAUUUUAAGAU 16

Sequence 17 BP; 6 A; 0 C; 1 G; 10 U; 0 other;

The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EARJ/COUP-TF-1, the GATA transcription factor gene, IRR-2 and/or the CAAT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha.

Ensymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin -

Claim 42; Page 128; 164pp; English.

McSwiggen J;

Pavco P,

Zwick M,

Blatt L,

WPI; 2000-647423/62.

99US-0129390.

12-APR-1999;

(RIBO-) RIBOZYME PHARM INC.

11-APR-2000; 2000WO-US09721

WO200061729-A2.

19-0CT-2000.

Homo sapiens.

erythropoietin; granulocyte colony stimulating factor;

Hammerhead ribozyme substrate #3149.

Ribozyme; erythropoie interferon alpha; ss.

(first entry)

16-FBB-2001

AAF06352;

schultz143-3.rng

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with a target sequence and contain at least one phosphoro(di)thicated like, having endomuclease activity. (A), and more generally any catalytic mucleic acid (A') that modulate expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or cancertion), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of constrogen receptor. Because of the high selectivity for targeted RNA, (A) and leo be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endomucleases are used with DNA). The combination of modifications in (A) improves resistance to mucleases, binding affinity and/or activity. AAA23503 to AAA2474 represent oestrogen receptor hairbin ribozyme sequences, and AAA2509 to AAA2502 represent corresponding target sequences, and AAA2519 to AAA2521 represent their corresponding target sequences. AAAA3509 to AAA2521 represent cherribozyme sequences. AAAA3529 to AAA2521 represent cherribozyme sequences. AAAA3529 to AAA2521 represent cherribozyme sequences. AAAA3529 to AAA2521 represent cherribozyme sequences. AAA35219 to AAA2521 represent cherribozyme sequences and antisense oligonucleotides used in the chempton.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead inbozyme; balrpin ribozyme; antiense oligomucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; sa
                                                                                                                The present invention describes nucleic acids (A) that interact
                        New nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer
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Haeberli P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 2 A; 0 C; 1 G; 14 T; 0 other;
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Zwick M, Jarvis T, Woolf T,
                                                                            Claim 77; Page 71; 148pp; English.
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98US-0103636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thompson JD,
Reynolds M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09954459-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-1998;
23-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA25363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 534
         8¥666666666666666666668¥¥¥¥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1. PCNA and Cyclin B1. Representative examples of ribozyme recognition sites are given in AAAB315 to AAAB6787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme is resistant to endomuclease activity and hence is efficient in restenosis treatment.
                                                                                                                                                                                                                                               New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDKI, PCNA and Cyclin B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.0%; Score 12.8; DB 1; Length 17
87.5%; Pred. No. 4.3e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beigelman L, McSwiggen JA, Karpeisky A,
Zwick M, Jarvis T, Woolf T, Haeberli P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 7 A; 2 C; 1 G; 7 T; 0 other;
                                                                                                                                                                              Robbins JM;
                                                                                                                                                                                                                                                                                                                         Example 1; Page 17; 109pp; English
                                                                                                                                                                              Barber JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1172 TITATTAGATAAATTT 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΗĐ
                                                                      99WO-US28772
                                                                                                        98US-0110954
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98US-0103636,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 TTTAATAGAGAATTT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA25179 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Conservative
                                                                                                                                                                            Tritz R, Welch PJ,
                                                                                                                                          (IMMG-) IMMGSOF INC
                                                                                                                                                                                                                 WPI; 2000-412314/35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thompson JD, Beig
Reynolds M, Zwic)
Matulic-Adamic J;
WO200032765-A2
                                                                    06-DEC-1999;
                                                                                                        04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                  08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9954459-A2
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 533
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Bellon L;

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The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di) thioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of controllate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endomucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/for activity. Analysisois to AAAA47478 to AAA2592 represent their corresponding target sequences. AAA2593 to AAAA5619 to AAAA5217 represent costrogen receptor harmmenhead ribozyme sequences. AAA2593 to AAAA5619 to AAAA56218 represent their corresponding target sequences. AAA26219 to AAAA5621 represent their corresponding target sequences. AAA26219 to AAAA5621 represent their corresponding target sequences. AAA26219 to AAAA5621 represent their corresponding target sequences. AAA26219 to AAAA6211 represent their corresponding target sequences and anisense oligonucleotides used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonuclectide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.0%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 4.3e+02; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 BP; 7 A; 0 C; 3 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exemplification of the present invention.
                                           Claim 77; Page 76; 148pp; English.
sequences, used to treat cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1538 AAGATGTTTTTATGTG 1553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA25365 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAAGTTTTTATGTG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-013248/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matulic-Adamic J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-APR-1999;
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23-JUN-1998;
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The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thloate (Ink, having endomuclases extravity. (A), and more generally any catalytic nucleic acid (A) that modulates expression of the oestrogen catalytic nucleic acid (A) that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or conformatium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of cataled cells, or for other conditions associated with levels of cataled cells, or for other conformation of the high selectivity for targeted RNA, (A) contrained to correlate inhibition of gene expression with categors, and as research reagents (for RNA, in the same way that confiction endomucleases are used with DNA). The combination of therapeutic modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA2393 to AAA2392 represent their corresponding target sequences, and AAA2393 to AAA2392 represent their corresponding target sequences, and AAA2393 to AAA2593 to AAA2593 represent ceptor receptor hairpin ribozyme sequences, and AAA2393 to AAA2593 represent ceptor receptor hairpin ribozyme sequences. AAA25619 to AAA2591 represent coher ribozyme sequences. AAA256219 to AAA2591 represent coher ribozyme sequences and antisense oligonucleotides used in the construction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endomuclease; anticancer; breast cancer; endometrium cancer; sex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acids that interact, and optionally cleave, target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
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Haeberli P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.0%; Score 12.8; DB 1;
87.5%; Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 17 BP; 6 A; 1 C; 3 G; 7 T; 0 other;
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is T, Woolf T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 77; Page 77; 148pp; English.
Claim 77; Page 77; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zwick M, Jarvis T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences, used to treat cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1539 AGATGTTTTTATGTGC 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA25366 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AAAGTTTTATGTGC 16
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98US-0103636.
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Reynolds M, Zwick M, Jarv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 87.5
Matches 14, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-013248/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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23-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 536
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The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the cestrogen receptor gene, are used to treat cancer (particularly of breast or reated cells, or for other conditions associated with levels of cestrogen receptor Because of the high selectivity for targeted RNA, (A) and also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagens (for RNA, in the same way that cestriction endonucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity, AAA23503 to AAA24747 represent cestrogen receptor corresponding target sequences, and AAA2503 to AAA2503 represent their corresponding target sequences. AAA2603 to AAA2503 represent cettor their corresponding target sequences. AAAA2603 to AAA2613 represent other ribozyme sequences. AAAA2619 to AAA2613 represent other ribozyme sequences and antisense oligonucleotides used in the exemplification of the present invention. \$88888888888888888888888888

Sequence 17 BP; 5 A; 2 C; 3 G; 7 T; 0 other;

ö 1.0%; Score 12.8; DB 1; Length 17; 87.5%; Pred. No. 4.3e+02; trive 0; Mismatches 2; Indels 1541 ATGITITITATGIGCIC 1556 AAGTITITATGTGCAC 17 14; Conservative Best Local Similarity N Query Match Matches ઠે å

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Gaps

RESULT 537 AAA25453/c

AAA25453 standard; DNA; 17 BP

19-JUL-2000 (first entry) AAA25453;

Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NQ:1951

Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; harmerhead ribozyme; haripin ribozyme; antisense oligomucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.

Homo sapiens

WO9954459-A2

28-OCT-1999,

98US-0082404. 98US-0103636. 20-APR-1998; 23-JUN-1998;

99WO-US08547

19-APR-1999;

(RIBO-) RIBOZYMB PHARM INC.

Bellon L; Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P; Matulic-Adamic J;

WPI; 2000-013248/01.

New mucleic acids that interact, and optionally cleave, target sequences, used to treat cancer

Claim 77; Page 79; 148pp; English.

The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thioate

The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen

New nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer

WPI; 2000-013248/01. Matulic-Adamic J;

Claim 77; Page 79; 148pp; English.

ö Destrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1952 Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; harmerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss. Gaps Bellon L; ö 1.0%; Score 12.8; DB 1; Length 17; 87.5%; Pred. No. 4.3e+02; tive 0; Mismatches 2; Indels Karpeisky A, Haeberli P; Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other; Thompson JD, Beigelman L, McSwiggen JA, Reynolds M, Zwick M, Jarvis T, Woolf T, exemplification of the present invention. 615 TACAAAAACAACAAA 630 AAA25454 standard; DNA; 17 BP 99WO-US08547. 17 TACAAAAAAAAAA 2 98US-0082404 98US-0103636 (RIBO-) RIBOZYME PHARM INC. 19-JUL-2000 (first entry) Local Similarity 87.5 les 14; Conservative Homo sapiens WO9954459-A2 19-APR-1999; 20-APR-1998; 23-JUN-1998; 28-OCT-1999. AAA25454; Query Match RESULT 538 Matches AAA25454, 88888888888888888888888 Š <u>8</u>

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creceptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of cestrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagens (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA21503 to AAA24747 represent costrogen receptor hammerhead ribozyme sequences, and AAA2478 to AAA2592 represent their corresponding target sequences. AAA2593 to AAA25107 to AAA2512 represent their receptor hairpin ribozyme sequences. AAAA56219 to AAAA5621 represent their corresponding target sequences. AAAA56219 to AAAA5621 represent their corresponding target sequences. AAAA56219 to AAAA5621 represent their ribozyme sequences and antisense oligonucleotides used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exemplification of the present invention.
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Query Match 1.0%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 4.3e+02; Matches 14; Conservative 0; Mismatches 2; Indels
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Gaps

615 TACAAAAACAACAAA 630 ||||||||||||||| 16 TACAAAAAAAAAA 1

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Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1985
                                                                                               Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonuclectide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.
                                 487/c
AAA25487 standard; DNA; 17 BP.
                                                                    (first entry)
                                                                                                                                       Homo sapiens
                                                                    19-JUL-2000
                                                     AAA25487;
                        RESULT 539
                                AAA25487
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98US-0082404. 98US-0103636. 99WO-US08547. (REBO-) RIBOZYME PHARM INC. WO9954459-A2 19-APR-1999; 20-APR-1998; 23-JUN-1998; 28-0CT-1999.

Bellon L; Karpeisky A, Haeberli P; Thompson JD, Beigelman L, McSwiggen JA, Reynolds M, Zwick M, Jarvis T, Woolf T, Matulic-Adamic J;

WPI; 2000-013248/01.

New nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer

Claim 77; Page 80; 148pp; English.

The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting

The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro (di)thioate catalytic endounclease activity. (A), and more generally any catalytic nucleic acid (A) that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or adometrium), in vivo or by transforming cells ex vivo and implanting trated cells, or for other conditions associated with levels of cestrogen receptor. Because of the high selectivity for targeted RNA, (A)

Claim 77; Page 97; 148pp; English.

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treated cells, or for other conditions associated with levels of ocstrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24747 represent cestrogen receptor hammerhead ribozyme sequences, and AAA25478 to AAA2592 represent their corresponding target sequences, and AAA25107 to AAA25018 represent their corresponding target sequences. AAA26219 to AAA26118 represent their corresponding target sequences. AAA26219 to AAA26211 represent their corresponding target sequences. AAA26219 to AAA26211 represent conter indoxyme sequences and antisense oligonucleotides used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease;
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                                                                                                                                                                                                                                                                                           1.0%; Score 12.8; DB 1; Length 17;
87.5%; Pred. No. 4.3e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beigelman L, McSwiggen JA, Karpeisky A,
Zwick M, Jarvis T, Woolf T, Haeberli P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anticancer; breast cancer; endometrium cancer; ss
                                                                                                                                                                                                                                                              Sequence 17 BP; 4 A; 3 C; 1 G; 9 T; 0 other;
                                                                                                                                                                                                         other ribozyme sequences and antisense ol:
exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                    1596 AAAAGTAAATATGAAA 1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA25991 standard; DNA; 17 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                   14; Conservative
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                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thompson JD, Beig
Reynolds M, Zwick
Matulic-Adamic J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA25991;
                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 540
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                                                                                                                                                                                                                                                                                                                                     Matches
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can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity handly AAA23503 to AAA2474 represent osetrogen receptor hammerhead riboxyme sequences, and AAA2474 to AAA2592 represent their corresponding target sequences, and AAA2593 to AAA2592 represent their receptor halrpin riboxyme sequences, and AAA26107 to AAA26108 represent their corresponding target sequences, and AAA26107 to AAA26118 represent their corresponding target sequences. AAA26219 to AAA26211 represent other riboxyme sequences and antisense oligonucleotides used in the exemplification of the present invention.
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Sequence 17 BP; 7 A; 1 C; 3 G; 6 T; 0 other;

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Gaps
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 Length 17;
                        2; Indels
Score 12.8; DB 1;
Pred. No. 4.3e+02;
0; Mismatches 2;
                                                 1055 TITATITAAGCAICAA 1070
 1.0%;
                                                                         16 TITATITIGAACAICAA 1
Query Match
Best Local Similarity 87.5
Matches 14; Conservative
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RESULT 541 ABA77913/c

ABA77913 standard; DNA; 17 BP.

ABA77913;

(first entry) 24-JAN-2002

BRCA1 mutation correcting oligonucleotide SEQ ID NO: 759.

Human, gene therapy, adenosine deaminase deficiency, p53; beta-globin; retinoblastoma; BRCA1; BRCA2, CFTR; cystic fibrosis; cancer; Factor V, cyclin-dependent kinase inhibitor 2A; CDRN2A; melanoma; APC; HEBA1; HBA2, adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOB; mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein B; LDLR; familial hypercolesterolaemia; UGT1; syndrome; APP; PSEN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presentlin-1; Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic; antilipemic; ss

Homo sapiens.

WO200173002-A2.

04-OCT-2001

27-MAR-2001; 2001WO-US09761

27-MAR-2000; 2000US-192176P. 27-MAR-2000; 2000US-192179P. 01-JUN-2000; 2000US-208538P. 30-OCT-2000; 2000US-244989P.

(UYDE) UNIV DELAWARE.

Kmiec KB, Gamper HB, Rice MC

WPI; 2001-639230/73.

Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification -

Claim 7; Page 90; 294pp; English.

The present invention provides single-stranded oligomucleotides which can be used for the targeted alteration of genomic sequences, where the oligomucleotide has at least one mismatch compared with the genomic

The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the

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sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, retinoblastoma, BRCAJ, BRCAZ, CTRR, cyclin-dependent kinase inhibitor 2A (CDKNZA), APC, Factor V, Factor VII, Factor IX, hemoglobin alpha locus I (HBAI), hemoglobin alpha locus 2 (HBAZ), MHI, MSH2, MSH6, MSH6, apolipoprotein E (ADOS), LDL receptor (LDIRA), UDP-Glucuronosyl transferase (UGT1), amyloid precursor protein (APC), presentlin-1 (PSENI) and presentlin-2 (PSENI). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia, halbelmer, s disease, malanoma, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting oligonucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDKN24; melanoma; APC; HEA21; HEA21; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOB; mismacth repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein B; LDLR; familial hyperchelesterolaemia; UGT1; syndrome; APP; FSRN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presentilin-1; Albeiner; g disease; cytostatic; antisickling; antianaemic; haemostatic;
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                                                                                                                                                                                                                                                                                                               1.0%; Score 12.8; DB 1; Length 17; 87.5%; Pred. No. 4.3e+02; ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BRCA1 mutation correcting oligonucleotide SEQ ID NO: 760.
                                                                                                                                                                                                                                                                            Sequence 17 BP; 6 A; 2 C; 3 G; 6 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABA77914 Standard; DNA; 17 BP.
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27-MAR-2000; 2000US-192179F.
01-JUN-2000; 2000US-208538F.
30-OCT-2000; 2000US-244889F.
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                                                                                                                                                                                                                                                                                                                                                      14; Conservative
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                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antilipemic; ss
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                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin.

retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A (DKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus (HML1, MSH2, MSH6, HRM6, APC), Pactor V, Factor VIII, Factor IX, haemoglobin alpha locus apolipoprotein B (APOB), LDL receptor (LDLR), UDP-glucuronosyltransferase (UGT1), amyloid precursor protein (APC), presenilin-1 (PSENI) and presenilin-2 (PSENI) and in the gene therrapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia, Alzheimer, disease, melanoma, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting oligonucleotides of the invention.
                                                                                                                                                                                                                                                     Query Match 1.0%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 4.3e+02; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APC mutation correcting oligonucleotide SEQ ID NO: 1459.
                                                                                                                                                                                                                             Sequence 17 BP; 6 A; 3 C; 2 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                     524 AATTTGAATTTCAGTA 539
                                                                                                                                                                                                                                                                                                                                                                                                                        ABA78613 standard; DNA; 17 BP
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ABA78613/
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Gaps ö Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDRN2A; melanoma; AFC; HEA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOB; mismatch repair; MSH2; MSH6; hyperlipidaemia; apollipoprotein B; LDLR; familial hypercholesterolasmia; UGT1; syndrome; APP; PSEN1; antisense; UDP-qiucuronosyltransferase; amyloid precursor protein; presentiin-1; Alzheimer; disease; cytostatic; antisickling; antianaemic; haemostatic;

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27-MAR-2000; 2000US-192176P.
27-MAR-2000; 2000US-192179P.
20-000; 2000US-208538P.
30-0CT-2000; 2000US-244989P.
27-MAR-2001; 2001WO-US09761.
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Oligonucleotide for targeted alterations of genetic sequences treating cystic fibrosis, comprises at least one mismatch and modification -

Rice MC.

Gamper HB,

Kmiec EB,

WPI; 2001-639230/73.

Claim 7; Page 133; 294pp; English.

The present invention provides single-stranded oligonucleotides which can

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be used for the targeted alteration of genomic sequences, where the oligomucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, thanks constant the following genes: adenosine deaminase, p53, beta-globin, crimoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2h (CDRTA3, APC, Factor VIII, Pactor IX, haemoglobin alpha locus (CDRTA3), hEH1, MSH6, MSH6, apolipoprotein E (APOB), LDL receptor (LDLR), UDP-glucuronosyltransferase (UGTI), amyloid preutursor protein (APC), presentlin-1 (PSENI) and presentlin-2 (PSEN2). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia, hampening disease, melanoma, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting oligomucleotides of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDNV2A; melanoma; APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE; mismatch repair; MSH2; MSH6; hyperlipideamia; apolipoprotein B; LDUE; familial hypercholesterolaemia; UGT1; syndrome; APP; PSRN1; antisense; UDP-glucuromosyltransferase; amyloid precursor protein; presentin-1; Alzheimer; disease; cytostatic; antisickling; antianaemic; haemostatic;
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                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.0%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 4.3e+02; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APC mutation correcting oligonucleotide SEQ ID NO: 1460.
                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 6 A; 4 C; 1 G; 6 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1577 TCTGATTGTATGGAAA 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA78614 standard; DNA; 17 BP.
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27-WAR-2000; 2000US-192199F.
01-JUN-2000; 2000US-208538P.
30-OCT-2000; 2000US-244989F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antilipemic; ss.
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The present invention provides single-stranded oligonuclectides which can be used for the targeted alteration of genomic sequences, where the CC oligonuclectide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin.

CC ECKNZA), APC, Pactor V, Pactor VII, Pactor IX, haemoglobin alpha locus (CDKNZA), APC, Pactor VII, Pactor IX, haemoglobin alpha locus (HDRA1), haemoglobin alpha locus (HOTI), amyloid precursor protein (APC), presentilar-I (PSRN) and precursor protein (APC), presentilar-I (PSRN) and precursor protein (APC), presentilar-I (PSRN) and precursor protein (APC), presentilar-I (PSRN). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, hemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia, Alzheimer's disease, The present sequence is one of the gene correcting oligonuclectides of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.0%; Score 12.8; DB 1; Length 17; 87.5%; Pred. No. 4.3e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 6 A; 1 C; 4 G; 6 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-SEP-2001 (first entry)
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Matches 14, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200130362-A2.
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AAH61737/C
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AAH61737/C
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Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent

Robbins JM, Tritz R;

WPI; 2001-300427/31.

Disclosure, Page 375, 408pp, English.

kinases

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The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme [1] which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (WMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule [11] comprising a promoter operably linked to a nucleic acid segment encoding [1]. [1] can have antipsoriatic, cytostatic, antiseborrheic, antidiabetic, antisickling, dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling, cytostathoric in the antidiabetic, antisickling, dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling, cleaves RNA encoding Gytokine involved in inflammation. [1] can be used in gene therapy. [1] and [11] are useful for treating proliferative keratosis, skin diseases such as psoriasis, atopic dermatities, actinic keratosis, also be used for treating proliferative eye diseases such as diabetic also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing scarring such as keloid, adhesion and hypertrophic or hypertrophic burn eventification of the companial event in the companial contraction and injection or hypertrophic burn event in the companial contraction and contracting and preventing and contraction and contracting and preventing event in the contraction and contracting an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus; SarA; staphylococcal accessory regulator A; agressory gene regulator; antibacterial; SarA inhibitor; virulence gene; staphylococcal infection; DNA footprinting; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus agr regulatory region footprinted region B2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.0%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 4.3e+02; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 7 A; 2 C; 1 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF56150 standard; DNA; 17 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYAR-) UNIV ARKANSAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-APR-2001
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The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids (a.g. a ribozyme or a DNazyme) an Inozyme (an endolytic nucleic acids (a.g. a ribozyme or a possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inozyme; G-claever; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin; a lymphoma; MHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CWA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
and assessing the binding of the candidate inhibitor to the SarA binding site of the agr locus. The identified inhibitors are useful for preventing and treating staphylococcal infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
                                                                                                       1.0%; Score 12.8; DB 1; Length 17; 87.5%; Pred. No. 4.3e+02; tive 0; Mismatches 2; Indels
                                                                    Sequence 17 BP; 9 A; 2 C; 1 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chowrira BM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 88; Page 72; 200pp; English.
                                                                                                                                                                                 1046 ATTTATGTATTTT 1061
                                                                                                                                                                                                                                                                                                          ABK00430 standard; RNA; 17 BP
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28-FEB-2000; 2000US-185516P.
06-MAR-2000; 2000US-187128P.
                                                                                                                                                                                                      09-FEB-2001; 2001WO-US04273
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(BLAT/) BLATT L.
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                             14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BEAT/) BLATT L.
(MCSW/) MCSWIGGEN J.
(CHOW/) CHOWRIRA B M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-607195/69.
                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                              ABK00430;
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                                                                                                           Query Match
Best Local S
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motif) pr an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a VGY motif). The CD20-tergetting nucleic acid is used to cleaving RNA with a VGY motif). The CD20-tergetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg^2t. Furthermore, it may be contacted with a cell to reduce associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leaveamia, B-cell , lymphoma, low-grade or follicular NHL, lymphocytic leukaemia, B-cell, bulky low-grade or follicular NHL, lymphocytic leukaemia, HIV (human (NHC), immunodeficiency virus) associated NHL, mantle-cell lymphoma (NHC), immunodeficiency virus) associated NHL, mantle-cell lymphoma (NHC), immunocytopaemia, and inflammatory arthropathy. The NOGO-targetting thrombocytopaemia, and inflammatory arthropathy. The NOGO-targetting divalent cation that is preferably Mg^2t. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and creatment may further comprise the use of one or more therapies.

CT treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies.

CT treat a patient disease, injury and cerebrovascular accident (CVA, certoxe), Alzheimer's disease, dementia, multiple sclerosis (MS), central nervous system (CNS) injury and cerebrovascular accident (CVA, certoxe), Alzheimer's disease, dementia, multiple sclerosis (MS), checotherapy-induced neuropathy, amd/or other neurodegenerative disease contrast contrast of the modulation of NOGO expression. The states and subject the neuropathy and or other neurodegenerative disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOG0; hammerhead ribozyme; brazyme; inozyme; d-cleaver; amberzyme; zinzyme; lywphoma; leukaemia; human immunodeficiency virus; HIV associated MHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.0%; Score 12.8; DB 1; Length 17; 37.5%; Pred. No. 4.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence is a hammerhead ribozyme of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 5 A; 2 C; 1 G; 9 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 909 CTCCTTTATTTCTAAG 924
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28-FEB-2000; 2000US-185516P.
06-MAR-2000; 2000US-187128P.
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Matches 6; Conservative
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Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
                                                                                                                                                                                                                                                 present sequence is a harmerhead ribozyme of the invention.
                                                                                                                                                                                                                                                           Sequence 17 BP; 5 A; 3 C; 1 G; 8 U; 0 other;
                              Chowrira BM;
                                                                  and central nervous system injury
                                                                           Claim 88; Page 73; 200pp; English.
     RIBOZYMB PHARM INC
                              Blatt L, McSwiggen J,
                    CHOW/) CHOWRIRA B M.
          BLATT L.
MCSWIGGEN J.
                                        WPI; 2001-607195/69
     (RIBO-)
               MCSW/)
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.; 0 Length 17; 2; Indels Score 12.8; DB 1; Pred. No. 4.3e+02; 0; Mismatches 2; 1.0%; Local Similarity 87.5 nes 14; Conservative Query Match Best Loca Matches

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Gaps

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ABK01316 standard; RNA; 17 BP. ABK01316; RESULT 549 ABK01316/c

12-MAR-2002 (first entry)

Human NOGO Inozyme #586.

Human, 88; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian;

muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; becal lymphoma; non-Hodgkin's lymphoma; MIL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; lumunocytoma; MC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; parkinson's disease; ataxia; Huntington's disease; creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

Homo sapiens.

Synthetic

WO200159103-A2.

16-AUG-2001

09-FEB-2001; 2001WO-US04273.

11-FEB-2000; 2000US-181797P. 28-FEB-2000; 2000US-185516P. 06-MAR-2000; 2000US-187128P.

RIBOZYME PHARM INC. BLATT L. MCSWIGGEN J. (RIBO-) | (BLAT/) | (MCSW/) |

(CHOW/) CHOWRIRA B M.

Chowrira BM; Blatt L, McSwiggen J,

WPI; 2001-607195/69.

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury

Claim 88; Page 87; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NDCO).

The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acids (leaving RNA with a NNA)

CC DNAzyme) an Inozyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a NGN treat a patient having a condition to associated with the level of CD20 in the presence of a divalent cation that is used to CD20 treat lymphoma, itelakamia, B-call lymphoma, low-grade or follicular NHL, lymphocytic leukaemia, HTV (human lymphoma, low-grade or follicular NHL, lymphocytic lymphoma (NHL), immunocytoma (INC), small B-call lymphocytic lymphoma (NHL), immunocytoma (INC), small B-call lymphocytic lymphoma (NHL), immunocytoma (INC), small B-call lymphocytic lymphoma, immunocytoma (INC), small B-call lymphocytic lymphoma, immunocytoma (INC), small B-call with the level of NGO gene in the presence of divalent cation that is preferably Mg²+. Furthermore, the nucleic acid may be used to treat central nervous system (CNS) injury and certivity of the cent accident (CNA, creat a patient having a condition associated with the level of NGO, genet treat ment may further comprise the use of one or more therapies. (INC) central nervous system (CNS) injury and certivity of the condition of streas, musuclay, and/or other neurodegeneration (CNA), chemotherapy-induced neuropathy, and/or other neurodegenerative (CNA), chemotherapy-induced is an inozyme of the inve

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                                                                                                                                                                                                                                                                                             Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOG0; hammerhead ribozyme; DNAzyme; inozyme; d-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphoma; leukaemia; human immunodeficiency virus; HIV associated NHL; lymphocytic leukaemia; MCL; immunocytoma; IMC; immune thrombocytopaemia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury
                                                          Gaps
                                                            ô
                               Length 17;
                                                          2; Indels
                            Query Match
1.0%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2;
   Sequence 17 BP; 5 A; 3 C; 1 G; 8 U; 0 other;
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                                                                                     1096 TAGAAGATGAATCATT 1111
                                                                                                                                                                                        BP
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28-FEB-2000; 2000US-185516P.
06-MAR-2000; 2000US-187128P.
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                                                                                                                16 TAGAAATGAATCAGT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIBOZYME PHARM INC.
                                                                                                                                                                                        ABK01612 standard; RNA; 17
                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                          Human NOGO G-Cleaver #68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blatt L, McSwiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RIBO-) RIBOZYME PHARM (BLAT/) BLATT L. (MCSW/) MCSWIGGEN J. (CHOW/) CHOWRIRA B M.
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                                                                                                                                                                                                                                               12-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                     ABK01612;
                                                                                                                                                            RESULT 550
ABK01612
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CC CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting conclude acid may be used to treat lymphoca, leukaemia, B-cell CT2 lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky lymphoma, low-grade or follicular NHL, mantle-cell lymphoma (NHL), bulky conversed or follicular NHL, mantle-cell lymphoma (NHL), includeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune (MCL), immunocytomania, and inflammatory arthropathy. The NGO-targetting concluded acid is used to cleave RNA of the NGCO gene in the presence of divalent cation that is preferably Mg^2+. Furthermore, the nucleic acid creat a patient having a condition associated with the level of NGCO. The creat may further comprise the use of one or more therapies. CC treatment may further comprise the use of one or more therapies. CC treatment may further comprise the use of one or more therapies. CC chemctherapy-induced neuropathy, amyotrophic lateral sclerosis (MS), chemctical micromassis (AS), chemctherapy-induced neuropathy, amyotrophic lateral sclerosis (MS). Parkinson's disease, muscular dystrophy, and/or other neurodegenerative disease content of NGCO extract neurodegenerative disease.
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Best Local Similarity 62.5%; Pred. No. 4.3e
Matches 10; Conservative 4; Mismatches
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28-FEB-2000; 2000US-185516P.
06-MAR-2000; 2000US-187128P.
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BLATT 1.
MCSWIGGEN J.
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(BLAT/) E
(MCSW/) N
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Chowrira BM

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The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NGCO).

Togulates expression of a neurite growth inhibitor gene (NGCO).

The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNAzwee) an Inozyme (an endolytic nucleic acid cleaving RNA with a NYR MORT motif), a G-cleaver (cleaving RNA with a NYR triplet), a zinzyme (cleaving RNA with a NGH notif), a G-cleaver (cleaving RNA with a NGH notif), a cleaving RNA with a NGH motif). The CD20-targetting nucleic acid is used (cleaving RNA with a YGY notif). The presence of a divident cation that is preferably MG'2'+. Furthermore, it may be contacted with a cell to reduce CD2 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting cucleic acid may be used to treat lymphoma, low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunocytoma (IMC), small b-cell lymphocytic lymphoma, immunocytoma (IMC), sm
                                                                                                                                                           Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
                                                                                                                                                                                                                                                                                                      Claim 88; Page 114; 200pp; English.
                                                                                                                                                                                                                                                  and central nervous system injury
                                                         Blatt L, McSwiggen J,
(CHOW/) CHOWRIRA B M.
                                                                                                                WPI; 2001-607195/69
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Sequence 17 BP; 9 A; 2 C; 3 G; 3 U; 0 other;

/ Match 1.0%; Score 12.8; DB 1; Length 17; Local Similarity 87.5%; Pred. No. 4.3e+02; hes 14; Conservative 0; Mismatches 2; Indels 0; Gaps Query Match Matches

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1276 AAGTACATTATTGTTT 1291 16 AAGTCCATTTTTGTTT

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ABV80683 standard; DNA; 17 BP RESULT 552

ABV80683;

03-JAN-2003 (first entry)

Human HTPL scanning oligonucleotide SEQ ID 1929.

Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.

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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL chartes an overall structure organization with the Patched protein. The shares an overall structure organization with the Patched protein. The shares at overtural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was important in regulating male germ cell development, and the HTPL gene was uspect to human chromosome lppi2.1. HTPL and its coding sequence are useful for diagnosing a disorder sused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture of a medicament for treatment or prevention of therapy and manufacture disorders of testis, or adrenal, adult and foctal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and mucleic acids are clinically useful dispancetic markers and potenial therapeutic agents for walmple from the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 5 A; 3 C; 2 G; 7 T; 0 other;
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                                                                                                                                                 30-JAN-2001; 2001WO-US00663.
30-JAN-2001; 2001WO-US00665.
30-JAN-2001; 2001WO-US00665.
30-JAN-2001; 2001WO-US00665.
30-JAN-2001; 2001WO-US00668.
30-JAN-2001; 2001WO-US00669.
23-MAX-2001; 2001US-0864761.
                                                                                                             28-JAN-2002; 2002EP-0001167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 87.5
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                 (AEOM-) AEOMICA INC
                     EP1229046-A2
                                                                 07-AUG-2002
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1457 GITTATTATGTACAAA 1472 17 ścirarcarciacaa Š a

03-JAN-2003 (first entry) ABV80685; ******

ABV80685 standard; DNA; 17 BP.

RESULT 553 ABV80685/ Human HTPL scanning oligonucleotide SEQ ID 1931.

Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.

Homo sapiens

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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the cwo. One of the single base pair changes introduces a premature stop codon in HTPL-S (single base pair changes introduces a premature stop codon in HTPL-S (single base pair changes introduces a premature stop codon in HTPL-S (single base) and the HTPL base pair changes an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was maportant in regulating and gram cell development, and the Gram are useful for diagnosing a disorder caused by mutation in HTPL, and in there, such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and feetal muscle or colon function. HTPL proteins and mucleic acids are clinically useful diagnostic markers and potential therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention.
male germ cell development; bone marrow; brain; kidney; lung; placenta;
prostate; skeletal muscle; colon; male infertility; cancer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL -
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                                                                                                                                                                                                                 30-JAN-2001; 2001WO-US00663.
30-JAN-2001; 2001WO-US00664.
30-JAN-2001; 2001WO-US00665.
30-JAN-2001; 2001WO-US00665.
30-JAN-2001; 2001WO-US00669.
30-JAN-2001; 2001WO-US00669.
23-WAY-2001; 2001US-0864761.
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Matches 14; Conservative
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                                                               Homo sapiens
                                                                                                   RP1229046-A2
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ID ABV8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV89851 to ABS98510; HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-1. (I for long). HTPL changes an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL sen important in regulating male aprendly imply that HTPL plays a role similar mapped to human chromosome 10pl2.1. HTPL and its coding sequence are mapped to human chromosome 10pl2.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in the such disorder associated with decreased expression or activity of human for the sorder included disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.0%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 4.3e+02; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human HTPL scanning oligonucleotide SEQ ID 4322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 6 A; 3 C; 3 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 317; 718pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1456 TGTTTATTATGTACAA 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABV83076 standard; DNA; 17 BP
                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00664.
30-JAN-2001; 2001WO-US00665.
30-JAN-2001; 2001WO-US00667.
30-JAN-2001; 2001WO-US00668.
30-JAN-2001; 2001WO-US00669.
93-MAY-2001; 2001US-0864761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 recrrareareracaa 1
                                                                                                                                             28-JAN-2002; 2002EP-0001167
                                                                                                                                                                                   30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-676582/73.
                                                                                                                                                                                                                                                                                                                                                                (ABOM-) AEOMICA INC
                                                                 BP1229046-A2.
                           Homo sapiens
                                                                                                     07-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABV83076;
                                                                                                                                                                                                                                                                                                                                                                                                         Zhan J;
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ABV83076
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Gaps

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Human POSHL1 scanning oligonucleotide SEQ ID NO 862

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Human, gene therapy, tumour suppressor; HTPL; chromosome 10p12.1,
human testis expressed Patched like protein; testis; adrenal; liver;
male germ cell development; bone marrow; brain; kidney; lung; placenta;
prostate; skeletal muscle; colon; male infertility; cancer; ss.
                                                                                                                                                                                                                                                                                                Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL -
                                                                                                                                                                                                                                                                                                                                             Example 2; Page 630; 718pp; English.
                                                                                                                                     30-JAN-2001; 2001WO-US00663.
30-JAN-2001; 2001WO-US00665.
30-JAN-2001; 2001WO-US00665.
30-JAN-2001; 2001WO-US00665.
30-JAN-2001; 2001WO-US00669.
23-MAY-2001; 2001WO-US0669.
                                                                                                                   28-JAN-2002; 2002EP-0001167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                    (AEOM-) AEOMICA INC.
                                                                                                                                                                                                                                                                             WPI; 2002-676582/73
                                                                         EP1229046-A2
                                                      Homo sapiens
                                                                                               07-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                          Zhan J;
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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall structure strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL so similar important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10pl2.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in the such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and such disorders include disorders of testis, or adrenal, adult and close the infertility and cancer. The present oligonucleotide was used in an example the infertility and cancer. The present oligonucleotide was used in an example the infertility and cancer. The present oligonucleotide was used in an example the properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 BP; 5 A; 3 C; 1 G; 8 T; 0 other;
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Query Match
                                                                         Matches
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                          Gaps
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1.0%; Score 12.8; DB 1; Length 17; 87.5%; Pred. No. 4.3e+02; ative 0; Mismatches 2; Indels
                     0
                                               603 TITATITGAATCTACA 618
                                                           TTTATTTGAATATCCA 16
                                                                                                                                ABV90149 standard; DNA; 17
                                                                                                         RESULT 556
ABV90149/c
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ABV90150 standard; DNA; 17

23-DEC-2002 (first entry)

ABV90149;

AXXXXX

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The invention relates to an isolated SH3 domain (POSH)-like signalling protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino acids (SI, ABBB3999), a sequence having 6% sequence identity to (SI), (SI), having 95% deviations, especially conservative substitutions or a fragment of the sequences comprising at least 8 contiguous amino acids. Human POSHL 1 is a prote-oncogene/oncogene product that functions as an adaptor protein that interacts with Rho family small GTBases as well as downstream components of the signal transduction pathway. (I) is useful for interaction of the signal transduction pathway. (I) is useful correcting (I) are useful for diagnosing, monitoring disease and tracting treating cancer, they useful in the development of vaccines and (II) is useful in gene therapy. (II) is useful for constructing microarrays which transgenic non-human animals capable of producing the procession and creating transgenic non-human animals capable of producing the process. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The present sequence did not form part of the printed specification, but is based on sequence information supplied to Derwent
                                      oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL-1, useful for treating disorders associated with decreased expression or activity of human POSHL1 -
                              Human, POSHL 1, SH3 domain, POSH-like signalling protein 1, oncoger
Rho GTPase, signal transduction, gene expression, cancer, vaccine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; SEQ ID NO 862; 60pp + Sequence Listing; English;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17 BP; 7 A; 2 C; 7 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1335 CAGTOTTGFCATTGCC 1350
                                                                        gene therapy; transgenic; ss.
                                                                                                                                                                                                             28-JAN-2002; 2002BP-0001165.
                                                                                                                                                                                                                                                                                                   2001WO-US00666
                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WC-US00668.
30-JAN-2001; 2001WC-US00669.
30-JAN-2001; 2001WC-US00670.
                                                                                                                                                                                                                                                                                                                                                                                             23-MAY-2001; 2001US-0864761
10-OCT-2001; 2001US-0328205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-684061/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AEOM-) AEOMICA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                    30-JAN-2001; 2
30-JAN-2001; 2
30-JAN-2001; 2
                                                                                                        Homo sapiens
                                                                                                                                           RP1239051-A2
                                                                                                                                                                                                                                                                      30-JAN-2001;
                                                                                                                                                                             11-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shannon M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 557
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Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;

Human CLCAl gene enzymatic nucleic acid #566.

(first entry)

02-JUL-2002 ABK56195;

B.

ABK56195 standard; RNA; 17

schultz143-3.rng

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RESULT 558
              ABK56195
                                      The invention relates to an isolated SH3 domain (POSH)-like signalling protein 1 (POSH 1) polypeptide (1), comprising a sequence of 730 amino acids (S1, ABB3399), a sequence having 65% sequence of 730 amino acids (S1) having 95% deviations, especially conservative substitutions or a fragment of the sequences comprising at least 8 contiguous amino acids. Human POSHL 1 is a proto-oncogene/oncogene product that functions as an adaptor procein that interacts with Rho family small GTPsess as well as adaptor procein that interacts with Rho family small GTPsess as well as components of the signal transduction pathway. (I) is useful for identifying a specific binding partner. (I) and nucleic acids (II) encoding (I) are useful for diagnosing, monitoring disease and treating cancer, they useful in the development of vaccines and (II) is useful in gene therapy. (II) is useful for constructing microarrays which transgenic non-human animals capable of producing the proteins. The present sequence is that of a scanning oligonucleotide useful in examples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the invention.

Note: The present sequence did not form part of the printed
specification, but is based on sequence information supplied to Derwent
by the Buropean Patent Office.
                                                                             nn, POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene; GTPase; signal transduction; gene expression; cancer; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL-1, useful for treating disorders associated with decreased expression or activity of human POSHL1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 1.0%; Score 12.8; DB 1; Length 17; Local Similarity 87.5%; Pred. No. 4.3e+02; les 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; SEQ ID NO 863; 60pp + Sequence Listing; English.
                                                    Human POSHL1 scanning oligonucleotide SEQ ID NO 863.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17 BP; 7 A; 2 C; 7 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                        30-7AN-2001, 2001WO-US00667.
30-7AN-2001, 2001WO-US00668.
30-7AN-2001, 2001WO-US00669.
30-7AN-2001, 2001WO-US00670.
23-MAY-2001, 2001US-0864761.
10-OCT-2001, 2001US-0328205.
                                                                                                        gene therapy; transgenic; ss.
                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00664.
30-JAN-2001; 2001WO-US00665.
30-JAN-2001; 2001WO-US00666.
                                                                                                                                                                                                              28-JAN-2002; 2002EP-0001165.
                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-684061/74.
                                                                                                                                                                                                                                                                                                                                                                                      (ABOM-) ABOMICA INC.
                                                                               Human; POSHL
                                                                                                                                                                                                                                         30-JAN-2001;
                                                                                                                                   Homo sapiens
                                                                                                                                                           BP1239051-A2
                          23-DEC-2002
                                                                                                                                                                                     11-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                 Shannon M;
 ABV90150;
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Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma

Claim 4; Page 63; 152pp; English.

Szymkowski DE;

Ayers D,

Thompson J, McSwiggen J, McKenzie T,

WPI; 2002-217145/27.

Grupe A;

09-AUG-2000; 2000US-224383P. 09-AUG-2001; 2001WO-US24970.

WO200211674-A2.

14-FEB-2002.

acetylcysteine Homo sapiens. (RIBO-) RIBOZYMB PHARM INC. (SYNT) SYNTEX USA LLC.

(THOM/) THOMPSON J.

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The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The mucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (CPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, thence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The mucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1, where the invention are also used as diagnostic tools to the presence of CLCA1 in a cell. This sequence represents an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 6 A; 1 C; 1 G; 9 U; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK56693 standard; RNA; 17 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enzymatic nucleic acid
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Matches
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ID ABK56
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Gaps

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1335 CAGTCTTGTCATTGCC 1350

Best Loc Matches

16 CACTCTTGTCCTTGCC 1

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Human, chloride channel calcium activated 1, CLCA1, 88; antiasthmatic; antiinflammatory, chronic obstructive pulmonary disease; COPD, asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
                                                                                                                                                                                                                                                                                                                          Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma -
                                                Human CLCAl gene enzymatic nucleic acid #1064.
                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 78; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    722 TTAATTTCAGGAATTG 737
                                                                                                                                                                                                              09-AUG-2000; 2000US-224383P.
                                                                                                                                                                                           09-AUG-2001; 2001WO-US24970.
                              (first entry)
                                                                                                                                                                                                                                                                          Thompson J, McSwiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Conservative
                                                                                                                                                                                                                                  (RIBO-) RIBOZYME PHARM (SYNT) SYNTEX USA LLC.
                                                                                                                                                                                                                                             SYNT ) SYNTEX USA LLC. (THOM/) THOMPSON J.
                                                                                                                                                                                                                                                                                                      WPI; 2002-217145/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                    WO200211674-A2.
                                                                                                             acetylcysteine
                                                                                                                                 Homo sapiens.
                              02-JUL-2002
                                                                                                                                                                       14-FEB-2002.
          ABK56693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17
                                                                                                                                                                                                                                                                                    Grupe A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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ID ABK:
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Szymkowski DE;

McKenzie T, Ayers D,

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The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaccutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic librosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corritosereoids, antibacterials, vaccinations, acetyloysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an expressents and expressents and example or the presence of CLCA1 RNA in a cell. This sequence represents and expressions and example of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 8 A; 4 C; 2 G; 3 U; 0 other;
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1.0%; Score 12.8; DB 1; Length 1
18.8%; Pred. No. 4.3e+02;
ve 3; Mismatches 2; Indels
enzymatic nucleic acid molecule of the invention.
                             Sequence 17 BP; 8 A; 4 C; 2 G; 3 U; 0 other;
                                                                                                                       1245 ITCAGATAAACAACAA 1260
                                                                                                                                                                                                                                ВР
                                                                                                                                         UCAGCUGAACAACAA 17
                                                                         68.88;
                                                                                                                                                                                                                              ABK56963 standard; RNA; 17
                                                                                                                                                                                                                                                                                            (first entry)
                                                                                         11, Conservative
                                                       Query Match
Best Local Similarity
Matches 11, Conserv
                                                                                                                                                                                                                                                                                           02-JUL-2002
                                                                                                                                                                                                                                                             ABK56963;
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ID ABK56
XX ABK56
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XX Humar
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                                                                                                                                      Gaps
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                                                                                                     1.0%; Score 12.8; DB 1; Length 1
87.5%; Pred. No. 4.38+02;
7ative 0; Mismatches 2; Indels
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Human CLCAl gene enzymatic nucleic acid #1334.

ABK56852,

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Gaps

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Length 17;

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The invention relates to enzymatic mucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by clearing RNA derived from the genes. The mucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic cibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to can amine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 kNA in a cell. This sequence represents an
                                                                              Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; attiinflamatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Szymkowski DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thompson J, McSwiggen J, McKenzie T, Ayers D,
                                        Human CLCAl gene enzymatic nucleic acid #1223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 84; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2000; 2000US-224383P.
                                                                                                                                                                                                                                                                                                                                       09-AUG-2001; 2001WO-US24970.
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        (RIBO-) RIBOZYMB PHARM (SYNT ) SYNTEX USA LLC. (THOM/) THOMPSON J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-217145/27.
                                                                                                                                                                                                                                                      WO200211674-A2
                                                                                                                                                                      acetylcysteine
                                                                                                                                                                                                              Homo sapiens.
  02-JUL-2002
                                                                                                                                                                                                                                                                                                 14-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grupe A;
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chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic; acetylcysteine.

09-AUG-2000; 2000US-224383P. 09-AUG-2001; 2001WO-US24970.

Szymkowski DE

WO200211674-A2 Homo sapiens.

14-FEB-2002.

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The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated I (CLCA1) genes by cleaving NAM derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (CDPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell, there, are useful for treatment of a patient having a condition cassociated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the creatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetyloysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an
Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antiinflamatory; chronic obstructive pulmonary diseases, COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic; acetylcysteine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bnzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma
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                                                                                                                                                                                                                                                                                                                                                                                       Thompson J, McSwiggen J, McKenzie T, Ayers D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 87; 152pp; English
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                                                                                                                                                                                                                                                                                 09-AUG-2000; 2000US-224383P.
                                                                                                                                                                                                                                            09-AUG-2001; 2001WO-US24970.
                                                                                                                                                                                                                                                                                                                   (RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                      (THOM/) THOMPSON J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                       WO200211674-A2.
                                                                                                                                      Homo sapiens.
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Best Local Similarity 37.5%; Pred. No. 4.3e+02;
Matches 6; Conservative 8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                Sequence 17 BP; 6 A; 1 C; 2 G; 8 U; 0 other;
                                                                                                                                                                                                                                                                                                  1136 TAGTAAATTTATTTA 1151
                                                                                                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                                                         ABK18668 standard; RNA; 17
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1D ABK18

AC ABK1.

XX AC ABK1.

XX COP-A:

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KW COPH:

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KW VULN

KW NULN
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Gaps

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Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;

Human CLCAl gene enzymatic nucleic acid #1429.

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The invention relates to enzymatic nucleic acid molecules that down capulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic through obversity bewell syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, connected with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the cample, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylycyteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an expressing an expression or expressions.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Enzymatic polymucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                    Szymkowski DE;
                                                                                                                                                                                         Thompson J, McSwiggen J, McKenzie T, Ayers D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 90; 152pp; English
(RIBO-) RIBOZYME PHARM INC.
(SYNT ) SYNTEX USA LLC.
(THOM/) THOMPSON J.
                                                                                                                                                                                                                                                                                                                                              WPI; 2002-217145/27.
                                                                                                                                                                                                                                                  Grupe A;
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angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; 88; Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
                                                                                                                                                                                                    Novel polynucleotide which down regulates expression of Ets-related gene, useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
                                                                                                                                                                 McSwiggen JA, Mclaughlin F, Randi AM;
                                                                                                                                                                                                                                                   Claim 4; Page 84; 149pp; English
                                                                                                                                                                Von Carlowitz I,
                                                                                                   16-MAY-2001; 2001WO-US15866
                                                                                                                     16-MAY-2000; 2000US-0572021
                                                                                                                                       (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                   WPI; 2002-082995/11.
                                                               WO200188124-A2.
                                              Homo sapiens
                                                                                 22-NOV-2001
                                                                                                                                                                Jarvis T,
                            amberzyme.
                                                                                                                                                                                                                                   syndrome
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The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Faury's saarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, the conditions allowed of tuberous sclerosis, port-wine stains, Sturge velgaris, angiotibroma of tuberous sclerosis, port-wine stains, Sturge Weber syndrome, Rippel-Trenaunay-Weber syndrome, Osler-Weber-rendu syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies or under conditions suitable for the treatment. Leukaemia or tumour conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or computence is treated by administering (I) to the patient in a cell, by contacting the cell with (I). (I) is useful for cleaving RNA of ERG gene, by contacting the cell with (I). (I) is useful for cleaving RNA of cation such as Mg2+. (I) is useful for reducing edigence to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect consuments method melecules within regulate expression of ERG such present nucleic acids, including antisense and ceryment may be no proposed to the expression of ERG such present nucleic acids, including antisense and ceryment conference of the present nucleic acids, including antisense and engance of the present nucleic acids, including antisense and engangement of the expression of the presence of ERG feed of the center of the presence of
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1.0%; Score 12.8; DB 1; Length 17; 87.5%; Pred. No. 4.3e+02; Live 0; Mismatches 2; Indels
                                                                 1235 AAATTTTCATTTCAGA 1250
                                   14; Conservative
                 West Local Similarity
   Query Match
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ABK18697 standard; RNA; 17
ABK18697/
ID ABK1
XX
AC ABK1
XX
DT 09-AI
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16 AAATTTTCATTTGACA

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(first entry) 09-APR-2002

ABK18697;

Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antipozoniatic; virucide; osteopathic; vulnerary; cancer; lymphome; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; atthitis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme, Human BRG G-cleaver ribozyme target sequence Seq ID No 1344. amberzyme.

WO200188124-A2. Homo sapiens.

22-NOV-2001.

16-MAY-2001; 2001WO-US15866.

16-MAY-2000; 2000US-0572021.

(RIBO-) RIBOZYME PHARM INC. (GLAX) GLAXO GROUP LTD.

Jarvis T, Von Carlowitz I, McSwiggen JA, Mclaughlin F,

WPI; 2002-082995/11.

Randi AM;

Novel polymucleotide which down regulates expression of Ets-related gene, useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome

Claim 4; Page 85; 149pp; English.

The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, tumour angiogenesis, diabetic retinopathy, macular degeneration, conditions edicated, myopic degeneration, arthritis, psoriasis, verruca vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge Weber syndrome, Isukaemia, osteoporosis and wound healing. (I) is useful for syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treatment apatient having a condition suitable for the treatment. The method comprises the use of one or more therapies under conditions suitable for the treatment Leukaemia or tumour conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or cell, by conteating (I) is useful for reducing ERG activity in a cell, by conteating (I) with RNM, in the presence of a divalent cation such as Mg2+. (I) is useful for diagnosis of conditions and diseased to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically caramine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically caramine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically caramine genetic drift and mutations within RNG gene or ERG fusion genes. ABRI7354-ABR22719 represent nucleic acides, including antisense and catacted PCR primers of the invention.

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Sequence 17 BP; 9 A; 0 C; 3 G; 5 U; 0 other;
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Gaps
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1.0%; Score 12.8; DB 1; Length 17; Similarity 87.5%; Pred. No. 4.3e+02;
                         2; Indels
                          0; Mismatches
               Local Similarity o...
  Query Match
                             Matches
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1171 TTTTATTAGATAAATT 1186 rrrrarracaracarr 17 ঠ 셤

Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds.

Tumour suppression related human fukutin oligo SEQ ID No 335.

ABT34698 standard; DNA; 17 BP.

ABT34698/c

12-JUN-2003 (first entry)

ABT34698;

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Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds.
                                                                                                                                                                                                                                       Tumour suppression related human fukutin oligo SEQ ID No 320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid, useful for treating viral diseal associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells
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                                    ABT34683 standard; DNA; 17 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-SEP-2002; 2002WO-IB04208.
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                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Felerman A, Amson R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                         ABT34683;
ABT34683/c
XX ABT34
XX ABT36
XX ABT36
XX ABT36
XX ABT36
XX ABT36
XX ABT37
X
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New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells

Tuijnder M;

Amson R,

relerman A,

WPI; 2003-313353/30.

(MOLE-) MOLECULAR ENGINES LAB 17-SEP-2001; 2001FR-0011978.

17-SEP-2002; 2002WO-IB04208

WO2003025175-A2. Homo sapiens.

27-MAR-2003.

Disclosure; Page 73; 720pp; French

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The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the nucleic acids, cells containing the nucleic acids, preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and sching acids in patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polymentical sequence represents a tumour suppression related human fukutin oligonucleotide of the invention.
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The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 155 consecutive nucleotides from the 17 mer sequence, a sequence with, after potinal alignment, at least 80 % identity to the 17 mer sequence, a sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as [anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and experience of the expression of the patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polypubcide sequence of the invention and be used in gene therapy. This polymorelide sequence represents a tumour suppression

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1.0%; Score 12.8; DB 1; Length 17;
87.5%; Pred. No. 4.3e+02;
ive 0; Mismatches 2; Indels
                                                         1462 TTATGTACAAATAGAT 1477
              Local Similarity 87.5%;
les 14; Conservative
                                                                                                                                                     ABT35053 standard; DNA; 17
                                                                                   17
     Query Match
                    Best Local
Matches
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ID ABT350
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Gaps ö

RESULT 566

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therapy, This polynucleotide sequence represents a tumm related human fukutin oligonucleotide of the invention

Sequence 17 BP; 5 A; 1 C; 3 G; 8 T; 0 other;

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